日 本 国 特 許 庁
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別紙添付の書類に記載されている事項は下記の出願書類に記載されている事項と同一であることを証明する。

This is to certify that the annexed is a true copy of the following application as filed with this Office

出 願 年 月 日
Date of Application: 2001年 8月24日

出 願 番 号
Application Number: 特願2001-254018
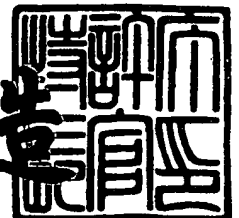
[ST.10/C]: [JP2001-254018]

出 願 人
Applicant(s): 旭化成株式会社

2002年 5月 7日

特 許 庁 長 官
Commissioner,
Japan Patent Office

及 川 耕 造

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出証番号 出証特2002-3032935

【書類名】	特許願
【整理番号】	X13-994
【提出日】	平成13年 8月24日
【あて先】	特許庁長官　殿
【国際特許分類】	C12N 15/00
	C12N 15/10
【発明の名称】	新規遺伝子
【請求項の数】	33

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【手数料の表示】

　　　　【予納台帳番号】　　015244

　　　　【納付金額】　　　　　21,000円

【提出物件の目録】

　　　　【物件名】　　　　　明細書　　1

　　　　【物件名】　　　　　図面　　1

　　　　【物件名】　　　　　要約書　　1

　　　　【包括委任状番号】　　0007328

【プルーフの要否】　　　要

【書類名】　　　　明細書

【発明の名称】　　新規遺伝子

【特許請求の範囲】

　【請求項１】　　以下の（ａ）または（ｂ）の精製されかつ単離されたタンパク質。

（ａ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなるタンパク質。

（ｂ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８において１若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつＮＦ−κＢ（Ｎｕｃｌｅａｒ　ｆａｃｔｏｒ　ｋａｐｐａ　Ｂ）を活性化する作用を有するタンパク質。

　【請求項２】　　請求項１記載のタンパク質とその全長にわたり９５％以上のアミノ酸配列の同一性を有するタンパク質であり、かつＮＦ−κＢを活性化する

作用を有する精製されかつ単離されたタンパク質。

　　【請求項３】　　以下の（ａ）または（ｂ）のタンパク質をコードするヌクレオチド配列を包含する単離されたポリヌクレオチド。

（ａ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなるタンパク質。

（ｂ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８において１若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつＮＦ－κＢを活性化する作用を有するタンパク質。

　　【請求項４】　　以下の（ａ）～（ｃ）のいずれかのポリヌクレオチド配列を含む単離されたポリヌクレオチド。

（ａ）配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、

７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、
９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１
４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３
２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５
０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６
７、１６９、１７１、１７３、１７５または１７７で表されるポリヌクレオチド
配列および該ポリヌクレオチド配列に相補的なポリヌクレオチド配列。

（ｂ）（ａ）のポリヌクレオチド配列を有するポリヌクレオチドとストリンジェ
ントな条件下でハイブリダイズし、かつＮＦ－κＢを活性化する作用を有するタ
ンパク質をコードするポリヌクレオチド配列。

（ｃ）配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、
２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、
４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、
７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、
９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１
４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３
２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５
０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６
７、１６９、１７１、１７３、１７５または１７７において、１若しくは複数個
のヌクレオチドが欠失、置換若しくは付加されたポリヌクレオチド配列からなり
、かつＮＦ－κＢを活性化する作用を有するタンパク質をコードするポリヌクレ
オチド配列。

　　【請求項５】　　請求項３記載のポリヌクレオチドと全長にわたり少なくとも
９５％以上の同一性を有し、かつＮＦ－κＢを活性化する作用を有するタンパク
質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

　　【請求項６】　　請求項４記載のポリヌクレオチドと全長にわたり少なくとも
９５％以上の同一性を有し、かつＮＦ－κＢを活性化する作用を有するタンパク
質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

　　【請求項７】　　請求項３～６のいずれか１項に記載のポリヌクレオチドによ

りコードされる精製されかつ単離されたタンパク質。

　　　【請求項８】　　請求項３～６のいずれか１項に記載のポリヌクレオチドを含有する組換えベクター。

　　　【請求項９】　　請求項８に記載の組換えベクターを含む形質転換された細胞。

　　　【請求項１０】　　請求項１または２に記載のタンパク質が膜タンパク質である場合における、請求項９記載の細胞の膜。

　　　【請求項１１】　　（ａ）請求項３～６のいずれか１項に記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

（ｂ）培地からタンパク質を回収する、

ことを含むタンパク質の製造方法。

　　　【請求項１２】　　（ａ）個体のゲノムにおける請求項１、２または７に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

（ｂ）該個体に由来するサンプル中での該タンパク質の発現量を分析する、

ことを含む、該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、発現するタンパク質の量が正常の２倍以上あるいは１／２以下の場合に病気であると診断する方法。

　　　【請求項１３】　　以下の工程を含むＮＦ－κＢ活性化の阻害活性または促進活性について化合物をスクリーニングする方法。

（ａ）ＮＦ－κＢを活性化するタンパク質をコードする遺伝子、およびＮＦ－κＢの活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

（ｃ）該形質転換された細胞と１あるいは複数個の候補化合物とを接触させる工程、

（ｄ）検出可能なシグナルを測定する工程、および

　　　　　　　　　出証特２００２－３０３２９３５

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程。

【請求項１４】　以下の工程を含む、医薬組成物を製造する方法。

（ａ）ＮＦ－κＢを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

（ｃ）該形質転換された宿主細胞と１あるいは複数個の候補化合物とを接触させる工程、

（ｄ）検出可能なシグナルを測定する工程、

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程、および

（ｆ）単離または同定された化合物を医薬組成物として最適化する工程。

【請求項１５】　ＮＦ－κＢ活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

（ａ）ＮＦ－κＢを活性化するタンパク質をコードする遺伝子、およびＮＦ－κＢの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

（ｂ）検出可能なシグナルを測定するための試薬
を含むキット。

【請求項１６】　請求項１、２または７に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

【請求項１７】　請求項１、２または７に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、請求項１、２または７記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

　　　　　　　　　　出証特２００２－３０３２９３５

【請求項１８】　ＮＦ－κＢの活性化タンパク質の発現を阻害する、請求項３～６のいずれか１項に記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

【請求項１９】　請求項１、２または７記載のタンパク質をコードするＲＮＡの開裂、またはＩκＢ（Ｉｎｈｉｂｉｔｏｒｙ　ｐｒｏｔｅｉｎ　ｏｆ　ＮＦ－κＢ）の分解へ導く経路のタンパク質をコードするＲＮＡの開裂により、ＮＦ－κＢの活性化を阻害するリボザイム。

【請求項２０】　炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される疾患の治療に有効な量の請求項１３記載の方法でスクリーニングされた化合物および／または請求項１６記載のモノクローナルまたはポリクローナル抗体および／または請求項１８記載のアンチセンスオリゴヌクレオチドおよび／または請求項１９記載のリボザイムを個体に投与することを含む疾患の治療法。

【請求項２１】ＮＦ－κＢの活性化を阻害または活性化するものとして請求項１４に記載の方法により製造された医薬組成物。

【請求項２２】　炎症、自己免疫疾患、癌またはウイルス性感染の治療のための請求項２１記載の医薬組成物。

【請求項２３】　ＮＦ－κＢ活性化に関連する疾患を患っている患者に請求項１４記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌およびウイルス性感染を治療する方法。

【請求項２４】　ＧＶＨＤ、皮膚疾患、ＩｇＡ腎炎、紫斑病性腎炎、増殖性腎炎または劇症肝炎の治療のための請求項２１記載の医薬組成物。

【請求項２５】　ＮＦ－κＢの阻害に関連する疾患を患っている患者に請求項１４記載の方法により製造された化合物を投与することからなるＧＶＨＤ、皮膚疾患、ＩｇＡ腎炎、紫斑病性腎炎、増殖性腎炎または劇症肝炎を治療する方法。

【請求項２６】　請求項１６記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

【請求項２７】　請求項１８記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

【請求項２８】　対象疾患が炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される、請求項２６または２７に記載の医薬組成物。

【請求項２９】　機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

（ａ）オリゴキャッピング法を用いて完全長ｃＤＮＡライブラリーを作製し、

（ｂ）完全長ｃＤＮＡおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに

（ｃ）シグナルを発するプラスミドを選択する、

方法。

【請求項３０】　配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２，２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるヌクレオチド配列のうち少なくとも１以上を含むデータセットおよび／または配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６および１７８で表されるアミノ酸配列のうち少なくとも１以上を含むデータセットを保存したコンピュータ読み込み可能媒体。

【請求項３１】　　請求項３０に記載の媒体上のデータと他のヌクレオチド配列および／または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／またはアミノ酸配列との同一性の算出を行う方法。

【請求項３２】　　配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７から選択されるヌクレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質。

【請求項３３】　　配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている不溶性基質。

【発明の詳細な説明】

【０００１】

【発明の属する技術分野】

本発明は、ＮＦ－κＢを活性化する作用を有するタンパク質、該タンパク質を

コードするＤＮＡ、該ＤＮＡの取得方法、該ＤＮＡを含有する組換えベクター、該組換えベクターを含有する形質転換体ならびに該タンパク質と特異的に反応する抗体に関する。また、本発明は、ＮＦ－κＢの過剰な活性化または阻害が関与する疾患の診断、治療または予防を行う際の本発明のタンパク質、ＤＮＡまたは抗体の使用に関する。

【０００２】

また本発明は、該タンパク質、ＤＮＡ、組換えベクターおよび形質転換体を用いて、ＮＦ－κＢの活性化を阻害または促進する物質をスクリーニングする方法に関する。

【０００３】

【従来の技術】

転写因子ＮＦ－κＢ（Ｎｕｃｌｅａｒ　ｆａｃｔｏｒ　ｋａｐｐａ　Ｂ）は、炎症や免疫反応に関与する種々の遺伝子の転写調節において重要な役割を果たしている。ＮＦ－κＢは、Ｒｅｌファミリーに属するホモあるいはヘテロ二量体からなり、無刺激の状態では、制御タンパク質であるＩκＢ（Ｉｎｈｉｂｉｔｏｒｙ　ｐｒｏｔｅｉｎ　ｏｆ　ＮＦ－κＢ）と複合体を形成することによりその核移行シグナルが覆い隠され、細胞質内で不活性型として存在する。

【０００４】

細胞にインターロイキン（ＩＬ）－１、腫瘍壊死因子（ＴＮＦ）－αなどのサイトカインの刺激が与えられると、ＩκＢはＩＫＫ（ＩκＢ　ｋｉｎａｓｅ）によってリン酸化され、ユビキチン化を経て２６Ｓプロテアソームにより分解される。これにより遊離されたＮＦ－κＢは核内に移行し、ＮＦ－κＢ結合配列と呼ばれているＤＮＡ配列に結合し、その制御下の遺伝子の転写を誘導する。ＮＦ－κＢによって発現調節を受けているとされている遺伝子は免疫グロブリン遺伝子の他、ＩＬ－１、ＴＮＦ－αなどの炎症性サイトカイン、インターフェロン、細胞接着因子等が知られており、ＮＦ－κＢはこれらの遺伝子の発現誘導を介して、炎症や免疫応答に関わっている。

【０００５】

ＮＦ－κＢの機能あるいは活性化を阻害することによって、炎症・免疫疾患や

その他の疾病、たとえば腫瘍増殖、に関与している多くの因子（タンパク質）の発現を抑制できる可能性があり、自己免疫や炎症を原因・症状とする疾病に対する医薬の有望な標的である〔たとえば、Ｃｌｉｎｉｃａｌ　Ｃｈｅｍｉｓｔｒｙ　４５，７－１７（１９９９）、Ｊ．Ｃｌｉｎ．Ｐｈａｒｍａｃｏｌ．３８，９８１－９９３（１９９８）、Ｇｕｔ　４３，８５６－８６０（１９９８）、Ｔｈｅ　Ｎｅｗ　Ｅｎｇｌａｎｄ　Ｊｏｕｒｎａｌ　ｏｆ　Ｍｅｄｉｃｉｎｅ　３６６，１０６６－１０７１（１９９７）、ＴｉＰＳ　４６－５０（１９９７）、Ｔｈｅ　ＦＡＳＥＢ　Ｊｏｕｒｎａｌ　９，８９９－９０９（１９９５）、Ｎａｔｕｒｅ　３９５，２２５－２２６（１９９８）、Ｓｃｉｅｎｃｅ　２７８，８１８－８１９（１９９７）、Ｃｅｌｌ　９１，２９９－３０２（１９９７）〕。

【０００６】

　細胞外からの情報は、何らかのシグナルの形に変えて、細胞膜を通過し細胞質をこえて核に到達し、標的遺伝子の発現を調節して細胞の応答が引き起こされる。そのため、細胞外の刺激からＮＦ－κＢの活性化に至る細胞内におけるシグナル伝達の仕組みを解明することは、自己免疫疾患や炎症症状を呈する疾患に対する新たな医薬の開発あるいは治療法の開発に非常に重要な手段を提供することとなり、極めて重要な意義を有している。

【０００７】

　しかしながら、細胞が一定の刺激を受けてからＮＦ－κＢの活性化に至るまでのシグナル伝達経路にはプロテインキナーゼなどの各種伝達分子が関わる多くのステップの存在が考えられ、従って、より効率的な創薬研究のためには、主要な役割を果たす伝達分子を明らかにした上でそれらに焦点をしぼった新しい薬物スクリーニング方法を確立することが望まれる。しかし、ＮＦ－κＢの活性化のメカニズムは上記ＩＫＫ、ユビキチン化酵素、２６Ｓプロテアソームの他、ＴＮＦ　ｒｅｃｅｐｔｏｒ　ａｓｓｏｃｉａｔｅｄ　ｆａｃｔｏｒ　２（ＴＲＡＦ２）やＮＦ－κＢ　ｉｎｄｕｃｉｎｇ　ｋｉｎａｓｅ（ＮＩＫ）などの幾つかのシグナル伝達分子が同定され、少しずつ解明されつつあるものの、いまだ不明な点が多く、新たなシグナル伝達分子の同定とより進んだＮＦ－κＢ活性化メカニズムの解明が望まれていた。

【０００８】

【発明が解決しようとする課題】

本発明の課題は、上記のように有用なＮＦ－κＢを活性化する作用を有する新規な遺伝子、タンパク質を見出し、これを医薬、診断薬、医療の分野で利用する方法を提供することにある。即ち、ＮＦ－κＢを活性化する作用を有する新規タンパク質、該タンパク質をコードするＤＮＡ、該ＤＮＡを含有する組換えベクター、該組換えベクターを含有する形質転換体、該タンパク質の製造方法、該タンパク質またはその部分ペプチドに対する抗体、該抗体の製造方法を提供する。

【０００９】

また、本発明は、該タンパク質、ＤＮＡ、組換えベクターおよび形質転換体を用いて、ＮＦ－κＢの活性化を阻害または促進する物質をスクリーニングする方法、該スクリーニング用キット、該スクリーニング方法もしくはスクリーニング用キットを用いて得られるＮＦ－κＢの活性化を阻害または促進する物質、該物質の製造方法、ＮＦ－κＢの活性化を阻害または促進する物質を含有している医薬などを提供する。

【００１０】

【課題を解決するための手段】

近年、生体内で発現している遺伝子を解析する手段として、ｃＤＮＡの配列をランダムに解析する研究が活発に行われており、このようにして得られたｃＤＮＡの断片配列がＥＳＴ（Expressed SequenceTag、たとえばhttp//www.ncbi.nlm.nih.gov/dbEST）として、データベースに登録され公開されている。しかし、ＥＳＴは配列情報のみであり、その機能を推定することは困難である。また、ＥＳＴはＵｎｉＧｅｎｅ（http//www.ncbi.nlm.nih.gov/UniGene）により整備され、これまでに約９２０００クラスターが登録されている。しかし、その多くは５'端ヌクレオチド配列を欠損しており、タンパク質翻訳開始部位を含まない。そのため、ｍＲＮＡのコード領域の決定を前提とするタンパク質の機能解析、プロモーターの解析による遺伝子発現制御の理解といった遺伝子機能の解析に直結しているとは言いがたい。

【００１１】

　一方、遺伝子の産物、すなわちタンパク質の機能を解明する方法の一つに、動物細胞を用いた一過性発現クローニング法がある（たとえば、実験医学別冊　遺伝子工学ハンドブック）。この方法は、動物細胞発現ベクターを用いて作製したｃＤＮＡライブラリーを、動物細胞にトランスフェクションすることで機能的なタンパク質を直接発現させ、このタンパク質が細胞に及ぼす生物活性を指標としてｃＤＮＡを同定、クローニングする方法である。この方法では、目的とするタンパク質産物に関する化学的情報（アミノ酸配列や分子量）をあらかじめ必要とせず、細胞内や培養液中に発現しているタンパク質の特異的生物活性を検出してｃＤＮＡクローンの同定を行うことができる。

【００１２】

　この発現クローニングを効率良く行なうためには、ｃＤＮＡライブラリーの作製方法を工夫する必要がある。なぜなら、従来より汎用されているｃＤＮＡライブラリー作製方法には幾つかの方法があるが（たとえばＧｕｂｂｌｅｒ−Ｈｏｆｆｍａｎの方法：Ｇｅｎｅ　２５（１９８３）オカヤマ−バーグの方法：Ｍｏｌ．Ｃｅｌｌ．Ｂｉｏｌ．２（１９８２））、これらの方法によって作製されたｃＤＮＡは、そのほとんどが５’末端ヌクレオチド配列を欠損したものであり、完全長（ｍＲＮＡの全ヌクレオチド配列を含む）であることは稀であるからである。その理由は、ｍＲＮＡからｃＤＮＡを作るのに使用する逆転写酵素が、完全長のｃＤＮＡを作る効率が必ずしも高くないからである。

【００１３】

　さらに、遺伝子の機能解析を試みるに際しては、完全長ｃＤＮＡをクローニングし、そこからタンパク質を発現させることが必須の要件である。従って、全体のクローンの中で、完全長のものの割合が高いライブラリーを作製することが、発現クローニングを効率良く行なうために必要であった。

【００１４】

　本発明者らは、上記課題を解決するために鋭意研究を重ねた結果、オリゴキャッピング法を用いて完全長ｃＤＮＡライブラリーを作製し、２９３ＥＢＮＡ細胞を用いたアッセイ系を完成し、該アッセイ系によりＮＦ−κＢを活性化する作用を有するタンパク質をコードする新規ＤＮＡ（ｃＤＮＡ）を単離することに成功

した。この新規ＤＮＡは、２９３ＥＢＮＡ細胞内で発現させることによりＮＦ−
κＢの活性化を誘発した。この結果は、この新規ＤＮＡがＮＦ−κＢの活性化に
関与するシグナル伝達分子であることを示しており、本発明を完成するに至った
。

【００１５】

すなわち、本発明は

（１）　以下の（ａ）または（ｂ）の精製され、かつ単離されたタンパク質。

（ａ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２
３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４
７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７
１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９
５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、
１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、
１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、
１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、
１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなる
タンパク質。

（ｂ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２
３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４
７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７
１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９
５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、
１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、
１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、
１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、
１７０、１７２、１７４、１７６または１７８において１若しくは複数個のアミ
ノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつＮＦ−κＢを
活性化する作用を有するタンパク質。

【００１６】

（２）　上記（１）記載のタンパク質とその全長にわたり少なくとも９５％のアミノ酸配列の同一性を有するタンパク質であり、かつＮＦ−κＢを活性化する作用を有する、精製されかつ単離されたタンパク質。

【００１７】

（３）　以下の（ａ）または（ｂ）のタンパク質をコードするヌクレオチド配列を包含する、単離されたポリヌクレオチド。

（ａ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなるタンパク質。

（ｂ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８において１若しくは複数個のアミノ酸が欠失、置換若しくは付加されたアミノ酸配列からなり、かつＮＦ−κＢを活性化する作用を有するタンパク質。

【００１８】

（４）　以下の（ａ）～（ｃ）のいずれかのポリヌクレオチド配列を含む単離さ

れたポリヌクレオチド。

（ａ）配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるポリヌクレオチド配列および該ポリヌクレオチド配列に相補的なポリヌクレオチド配列。

（ｂ）（ａ）のポリヌクレオチド配列を有するポリヌクレオチドとストリンジェントな条件下でハイブリダイズし、かつＮＦ－κＢを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

（ｃ）配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７において、１若しくは複数個のヌクレオチド配列が欠失、置換若しくは付加されたポリヌクレオチド配列からなり、かつＮＦ－κＢを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列。

【００１９】

（５）　上記（３）記載のポリヌクレオチドと全長にわたり少なくとも９５％以上の同一性を有し、かつＮＦ－κＢを活性化する作用を有するタンパク質をコー

ドするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

（６）　上記（４）記載のポリヌクレオチドと全長にわたり少なくとも９５％以上の同一性を有し、かつＮＦ－κＢを活性化する作用を有するタンパク質をコードするポリヌクレオチド配列を包含する単離されたポリヌクレオチド。

（７）　上記（３）～（６）のいずれか１つに記載のポリヌクレオチドによりコードされる精製されかつ単離されたタンパク質。

（８）　上記（３）～（６）のいずれか１つに記載のポリヌクレオチドを含有する組換えベクター。

（９）　上記（８）に記載の組換えベクターを含む形質転換された細胞。

（１０）　上記（１）または（２）に記載のタンパク質が膜タンパク質である場合における、上記（９）記載の細胞の膜。

【００２０】

（１１）　（ａ）上記（３）～（６）のいずれか１つに記載の単離されたポリヌクレオチドがコードするタンパク質を発現する条件下で該ポリヌクレオチドを含有する形質転換された細胞を培養し、

（ｂ）培地からタンパク質を回収する、

ことを含む、タンパク質の製造方法。

【００２１】

（１２）　（ａ）個体のゲノムにおける上記（１）、（２）または（７）に記載のタンパク質をコードするヌクレオチド配列中の変異の存在または不存在を決定し、および／または

（ｂ）該個体に由来するサンプル中での該タンパク質の発現量を分析する、

ことを含む該個体における該タンパク質の発現または活性に関連した、該個体における疾病または疾病への感受性の診断方法であって、発現するタンパク質の量が正常の２倍以上の場合あるいは１／２以下の場合に病気であると診断する方法。

【００２２】

（１３）　以下の工程を含むＮＦ－κＢ活性化の阻害活性または促進活性ついて化合物をスクリーニングする方法。

（ａ）ＮＦ－κＢを活性化するタンパク質をコードする遺伝子およびＮＦ－κＢの活性化に対応した、検出可能シグナルを提供しうる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された細胞を培養する工程、

（ｃ）該形質転換された細胞と１あるいは複数個の候補化合物とを接触させる工程、

（ｄ）検出可能なシグナルを測定する工程、および

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程。

【００２３】

（１４）　以下の工程を含む、医薬組成物を製造する方法。

（ａ）ＮＦ－κＢを活性化する作用を有するタンパク質をコードする遺伝子、および検出可能なシグナルを提供しうる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で該形質転換された宿主細胞を培養する工程、

（ｃ）該形質転換された宿主細胞と１あるいは複数個の候補化合物とを接触させる工程、

（ｄ）検出可能なシグナルを測定する工程、

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離もしくは同定し、および／または該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離もしくは同定する工程、および

（ｆ）単離または同定された化合物を医薬組成物として最適化する工程。

【００２４】

（１５）　ＮＦ－κＢ活性化の阻害活性または促進活性について化合物をスクリーニングするためのキットであって、

（ａ）ＮＦ－κＢを活性化するタンパク質をコードする遺伝子、およびＮＦ－κ

Ｂの活性化後、検出可能なシグナルを提供しうる成分により形質転換された細胞、および

（ｂ）検出可能なシグナルを測定するための試薬
を含むキット。

【００２５】

（１６）　上記（１）、（２）または（７）に記載のタンパク質に特異的に結合するモノクローナルあるいはポリクローナル抗体。

（１７）　上記（１）、（２）または（７）に記載のタンパク質を抗原あるいはエピトープ含有フラグメントとして非ヒト動物に投与することからなる、上記（１）、（２）または（７）記載のタンパク質に特異的に結合するモノクローナルまたはポリクローナル抗体の製造方法。

（１８）　ＮＦ－κＢの活性化タンパク質の発現を阻害する、上記（３）～（６）のいずれか１つに記載のポリヌクレオチドに相補的なアンチセンスオリゴヌクレオチド。

（１９）　上記（１）、（２）または（７）記載のタンパク質をコードするＲＮＡの開裂、またはＩκＢの分解へ導く経路のタンパク質をコードするＲＮＡの開裂により、ＮＦ－κＢの活性化を阻害するリボザイム。

【００２６】

（２０）　炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される疾患の治療に有効な量の上記（１３）記載の方法でスクリーニングされた化合物および／または上記（１６）記載のモノクローナルまたはポリクローナル抗体および／または上記（１８）記載のアンチセンスオリゴヌクレオチドおよび／または上記（１９）記載のリボザイムを個体に投与することを含む疾患の治療法。

（２１）ＮＦ－κＢの活性化を阻害または活性化するものとして上記（１４）に記載の方法により製造された医薬組成物。

（２２）　炎症、自己免疫疾患、癌およびウイルス性感染の治療のための上記（２１）記載の医薬組成物。

（２３）　ＮＦ－κＢ活性化を患っている患者に上記（１４）記載の方法により製造された医薬組成物を投与することからなる炎症、自己免疫疾患、癌およびウ

イルス性感染を治療する方法。

（24）　ＧＶＨＤ、Ｔｏｘｉｃ　ｅｐｉｄｅｒｍａｌ　ｎｅｃｒｏｌｙｓｉｓ（ＴＥＮ）などの皮膚疾患、ＩｇＡ腎炎、紫斑病性腎炎、ループス腎炎などの増殖性腎炎および劇症肝炎の治療のための上記（21）記載の医薬組成物。

【0027】

（25）　ＮＦ－κＢの阻害を患っている患者に上記（14）記載の方法により製造された医薬組成物を投与することからなるＧＶＨＤ、Ｔｏｘｉｃ　ｅｐｉｄｅｒｍａｌ　ｎｅｃｒｏｌｙｓｉｓ（ＴＥＮ）などの皮膚疾患、ＩｇＡ腎炎、紫斑病性腎炎、ループス腎炎などの増殖性腎炎および劇症肝炎を治療する方法。

（26）　上記（16）記載のモノクローナルまたはポリクローナル抗体を有効成分として含有する医薬組成物。

（27）　上記（18）記載のアンチセンスオリゴヌクレオチドを有効成分として含有する医薬組成物。

（28）　対象疾患が炎症、自己免疫疾患、感染症および癌疾患からなる群から選択される、上記（26）または（27）に記載の医薬組成物。

【0028】

（29）　機能を有する新規遺伝子の取得方法であり、少なくとも以下の工程を含む方法。

（ａ）オリゴキャッピング法を用いて完全長ｃＤＮＡライブラリーを作製し、

（ｂ）完全長ｃＤＮＡおよび該機能を有するタンパク質の存在を示すシグナルを発する因子を含有するプラスミドを細胞中にコトランスフェクションし、さらに

（ｃ）シグナルを発するプラスミドを選択する。

【0029】

（30）　配列番号2、4、6、8、10、12、14、16、18、20、22、24、26、28、30、32、34、36、38、40、42、44、46、48、50、52、54、56、58、60、62、64、66、68、70、72、74、76、78、80、82、84、86、88、90、92、94、96、98、100、102、104、106、108、110、112、114、116、118、120、122、124、126、128、130、

１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、
１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、
１６７、１６９、１７１、１７３、１７５および１７７で表されるヌクレオチド
配列のうち少なくとも１以上を含むデータセットおよび／または配列番号１、３
、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９
、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３
、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７
、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０
１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１
９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３
７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５
６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７
４、１７６および１７８で表されるアミノ酸配列のうち少なくとも１以上を含む
データセットを保存したコンピュータ読み込み可能媒体。

【００３０】

（３１）上記（３０）に記載の媒体上のデータと他のヌクレオチド配列および／
または他のアミノ酸配列のデータを比較して他のポリヌクレオチド配列および／
またはアミノ酸配列との同一性の算出を行う方法。

【００３１】

（３２）　配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２
２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４
６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７
０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９
４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、
１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、
１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、
１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、
１６７、１６９、１７１、１７３、１７５または１７７から選択されるヌクレオ
チド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶性基質

。

【００３２】

（３３）　配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１
、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５
、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９
、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３
、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１
３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３
１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４
９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６
８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列から
選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固定されている
不溶性基質。

【００３３】

　　まず、本発明の基本的特徴を更に明らかにするために、本発明の完成に至る経
緯を追いながら、本発明について説明する。ＮＦ−κＢを活性化する作用を有す
る新規遺伝子を取得する目的で、実施例に示すように、以下の実験を実行した。
まずヒト正常肺線維芽細胞（三光純薬株式会社より購入）より調製したｍＲＮＡ
より、オリゴキャッピング法によって完全長ｃＤＮＡを作製し、該ｃＤＮＡをベ
クターｐＭＥ１８Ｓ−ＦＬ３（GenBank Accession AB009864）に組み込んだ完全
長ｃＤＮＡライブラリーを作製した。次に、該ｃＤＮＡライブラリーを大腸菌に
導入し、１クローンずつプラスミドを調製した。次に、２９３−ＥＢＮＡ細胞（
インビトロジェン社）に、ルシフェラーゼをコードするDNAを含有するｐＮＦκ
Ｂ−Ｌｕｃレポータープラスミド（ＳＴＲＡＴＡＧＥＮＥ社）と上記の完全長ｃ
ＤＮＡプラスミドとを共導入した。そして、２４時間あるいは４８時間培養後、
ルシフェラーゼ活性を測定し、ルシフェラーゼ活性が対照実験（完全長ｃＤＮＡ
の代わりに、ベクターｐＭＥ１８Ｓ−ＦＬ３を入れた細胞）と比べて有意に上昇
している（対照実験と比べてルシフェラーゼ活性が１０倍以上の値を示した）プ
ラスミドを選抜し、該プラスミドにクローニングされているｃＤＮＡの全ヌクレ

オチド配列を決定した。このようにして得られたｃＤＮＡによりコードされるタンパク質は、該タンパク質がＮＦ－κＢの活性化に関与するシグナル伝達分子であることを示している。

　次に、以下に本発明について詳細に説明する。

　【００３４】

　配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８のアミノ酸配列に関連して、本発明は、以下のタンパク質を提供する。

　（ａ）上記アミノ酸配列を含むタンパク質。

　（ｂ）上記アミノ酸配列の１つを有するペプチド。

　（ｃ）ＮＦ－κＢを活性化し、かつ上記アミノ酸配列において、１以上のアミノ酸の削除、置換または付加を有するタンパク質。

　（ｄ）その全長にわたり配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８のアミノ酸配列に少なくとも９５％、好ましくは９７～９９％の同一性を有するアミノ酸配列を

含むタンパク質。

【００３５】

　“同一性”とは、当該技術で知られているとおり、配列を比較することにより決定される、２以上のタンパク質あるいは２以上のポリヌクレオチドの間の関係である。当該技術で“同一性”とは、タンパク質またはポリヌクレオチド配列の間の適合によって、あるいは場合によっては、一続きのそのような配列間の適合によって決定されるような、タンパク質またはポリヌクレオチド配列の間の配列相関性の程度を意味する。“同一性”および“類似性”は、既知の方法により容易に決定できる。同一性を決定する好ましい方法は、試験する配列間で最も長く適合するように設計される。同一性および類似性を決定するための方法は、公に利用可能なプログラムにコードされている。相同性決定には、Altschulらによる BLAST (Basic Local Alignment Search Tool) プログラム（たとえば、Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ., J. Mol. Biol., 215: p403-410 (1990), Altschyl SF, Madden TL, Schaffer AA, Zhang J, Miller W, Lipman DJ., Nucleic Acids Res. 25: p3389-3402 (1997))を利用し決定することができる。

【００３６】

　上記した配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８に記載されたアミノ酸配列からなるタンパク質がＮＦ−κＢを活性化する作用を有することは、本願明細書実施例に記載の通りである。

【００３７】

　配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２，１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７のポリヌクレオチドに関連して、本発明は、また以下の単離されたポリヌクレオチドを提供する。

（ａ）上記配列に少なくとも９５％、好ましくは９７－９９％の同一性を有するヌクレオチド配列を含むポリヌクレオチド。

（ｂ）上記配列のポリヌクレオチド。

（ｃ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８のアミノ酸配列に少なくとも９５％、好ましくは９７～９９％の同一性を有するアミノ酸配列を有するタンパク質をコードするヌクレオチド配列を有するポリヌクレオチド。

【００３８】

　上記ヌクレオチド配列に含まれるヌクレオチド配列に同一またはほとんど同一なポリヌクレオチドは、本発明のタンパク質をコードする全長ｃＤＮＡ及びゲノムクローンまたは上記配列に対応する相同性の高い他の遺伝子のｃＤＮＡまたはゲノムクローンを単離するためのハイブリダイゼーションプローブとして、また

は核酸増幅反応のためのプライマーとして使用してもよい。代表的には、これら
のヌクレオチド配列は、上記配列に７０％同一であり、好ましくは、８０％同一
であり、より好ましくは９０％同一であり、最も好ましくは、９５％同一である
。プローブまたはプライマーは、一般的には少なくとも１５ヌクレオチドを含有
し、好ましくは３０ヌクレオチドを含有し、５０ヌクレオチドを含有してもよい
。特に好ましいプローブは、３０〜５０ヌクレオチドを有する。特に好ましいプ
ライマーは、２０〜２５ヌクレオチドを有する。

【００３９】

本発明のポリヌクレオチドは、ＤＮＡの形態（たとえば、ｃＤＮＡおよびクロ
ーニングによって得られるか、あるいは合成的に生成されるゲノムＤＮＡを含む
）であってもよく、ＲＮＡ（たとえばｍＲＮＡ）の形態であってもよい。該ポリ
ヌクレオチドは、二本鎖であっても、一本鎖であってもよい。二本鎖の場合は、
二本鎖ＤＮＡ、二本鎖ＲＮＡまたはＤＮＡ：ＲＮＡのハイブリッドであってもよ
い。一本鎖の場合は、センス鎖（コード鎖としても知られる）であっても、アン
チセンス鎖（非コード鎖としても知られる）であってもよい。

【００４０】

当業者であれば、公知の方法を用いてこのタンパク質中のアミノ酸の置換など
を適宜行い、配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２
１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４
５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６
９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９
３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１
１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１
３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１
４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１
６８、１７０、１７２、１７４、１７６または１７８に記載のアミノ酸配列を有
するタンパク質と同様にNF−κBを活性化する作用を有するタンパク質を作製する
ことが可能である。一つの方法としては、該タンパク質をコードするＤＮＡに対
して、慣用の突然変異誘発法を使用する方法がある。別の方法としてはたとえば

部位特異的変異法（たとえば宝酒造株式会社のＭｕｔａｎ－Ｓｕｐｅｒ　Ｅｘｐ
ｒｅｓｓ　Ｋｍ　キット）が挙げられる。また、タンパク質のアミノ酸の変異は
自然界においても生じうる。このようにアミノ酸の欠失、置換、付加により配列
番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、
２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、
５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、
７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、
９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１
１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１
３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１
５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１
７２、１７４、１７６または１７８のタンパク質に対してアミノ酸配列が変異し
た変異体であって、ＮＦ－κＢを活性化する作用を有するタンパク質及び該タン
パク質をコードするＤＮＡも本発明に含まれる。変異の数は、好ましくは１０ま
で、より好ましくは５まで、最も好ましくは３までが好ましい。

　　　【００４１】

　アミノ酸置換の例としては、保存的置換が好ましく、具体的には以下のグルー
プ内での置換が挙げられる。（グリシン、アラニン）（バリン、イソロイシン、
ロイシン）（アスパラギン酸、グルタミン酸）（アスパラギン、グルタミン）（
セリン、トレオニン）（リジン、アルギニン）（フェニルアラニン、チロシン）
。

　　　【００４２】

　当業者であれば、ハイブリダイゼーション技術などを用いて配列番号１、３、
５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、
３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、
５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、
７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１
、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９
、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７

、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６

、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４

、１７６または１７８で表されるアミノ酸配列からなるタンパク質をコードする

ＤＮＡ（たとえば配列番号２）またはその一部を基に、これと類似性の高いＤＮ

Ａを単離して、該ＤＮＡから配列番号１、３、５、７、９、１１、１３、１５、

１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、

４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、

６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、

８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０

９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２

７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４

５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６

４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表される

アミノ酸配列からなるタンパク質と同様にNF-κBを活性化する作用を有するタン

パク質を得ることも通常行い得ることである。このように上記した配列番号１、

３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２

９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５

３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７

７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１

０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１

１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１

３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１

５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１

７４、１７６または１７８で表されるアミノ酸配列のタンパク質と高い同一性を

有するタンパク質であって、ＮＦ−κＢを活性化する作用を有するタンパク質も

本発明のタンパク質に含まれる。高い同一性とは、上記配列番号１、３、５、７

、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、

３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、

５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、

８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８であらわされるアミノ酸配列の全長にわたり少なくとも９０％、好ましくは、少なくとも９７－９９％の同一性を有するアミノ酸配列を示す。

【００４３】

本発明のタンパク質としては、ヒトや哺乳動物のあらゆる細胞や組織に由来する天然のタンパク質でもよく、化学合成タンパク質であってもよく、また遺伝子組換え技術によって得られたタンパク質でもよい。タンパク質は糖鎖やリン酸化などの翻訳後修飾は受けていても受けていなくても良い。

【００４４】

本発明は、上記で示される本発明のタンパク質をコードするポリヌクレオチドである。上記の配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列としてより具体的には、たとえば配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２，２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２，１１４

、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるヌクレオチド配列が挙げられる。ＤＮＡはｃＤＮＡのほか、ゲノムＤＮＡ、化学合成ＤＮＡも含まれる。遺伝暗号の縮重に従い、遺伝子から生産されるタンパク質のアミノ酸配列を変えることなく配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列からなるタンパク質をコードするヌクレオチド配列の少なくとも１つのヌクレオチドを他の種類のヌクレオチドに置換することができる。従って、本発明のＤＮＡはまた、遺伝暗号の縮重に基づく置換によって変換されたヌクレオチド配列も含有する。このようなＤＮＡは、公知の方法により合成することができる。

【００４５】

本発明のＤＮＡは、配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるヌ

クレオチド配列からなるＤＮＡとストリンジェントな条件下でハイブリダイズし、かつＮＦ－κＢを活性化する作用を有するタンパク質をコードするＤＮＡも含まれる。ストリンジェントな条件とは、当業者には十分理解できることであり、たとえば、Ｔ．Ｍａｎｉａｔｉｓらの実験操作書（Ｍｏｌｅｃｕｌａｒ　Ｃｌｏｎｉｎｇ　Ａ　Ｌａｂｏｒａｔｏｒｙ　Ｍａｎｕａｌ，Ｃｏｌｄ　Ｓｐｒｉｎｇ　Ｈａｒｂｏｒ　Ｌａｂｏｒａｔｏｒｙ　１９８２、１９８９）に従えば容易に実施できる。

【００４６】

　すなわち、ストリンジェントな条件とは、３０％ホルムアミドを含むハイブリダイゼーション溶液中（５×ＳＳＣ（０．７５ＭのＮａＣｌ、７５ｍＭのクエン酸三ナトリウム）、５×デンハルト溶液、０．５％ＳＤＳ、１００μｇ／ｍｌの変性せん断サケ精子ＤＮＡ）で３７℃のインキュベーションを一晩行い、その後２×ＳＳＣ、０．１％ＳＤＳ中、室温で１０分の洗浄を３回行い、次いで１×ＳＳＣ、０．１％ＳＤＳ中、３７℃で１０分の洗浄を２回行う条件である（低ストリンジエンシー）。より好ましい条件は、４０％ホルムアミドを含むハイブリダイゼーション溶液中で４２℃のインキュベーションを一晩行い、その後２×ＳＳＣ、０．１％ＳＤＳ中、室温で１０分の洗浄を３回行い、次いで０．２×ＳＳＣ、１％ＳＤＳ中、４２℃で１０分の洗浄を２回行う条件である（中ストリンジエンシー）。最も好ましい条件は、５０％ホルムアミドを含むハイブリダイゼーション溶液中で４２℃のインキュベーションを一晩行い、その後２×ＳＳＣ、０．１％ＳＤＳ中、室温で１０分の洗浄を３回行い、次いで０．２×ＳＳＣ、０．１％ＳＤＳ中、５０℃で１０分の洗浄を２回行う条件である（高ストリンジエンシー）。この際、得られたＤＮＡは、ＮＦ－κＢを活性化する作用を有するタンパク質をコードすることが必須である。

【００４７】

　本発明は、上記（３）あるいは（４）のポリヌクレオチドのヌクレオチド配列と高い類似性を有し、かつＮＦ-κＢを活性化する作用を有するタンパク質をコードするヌクレオチドを含むポリヌクレオチドを含む。代表的には、これらのヌクレオチド配列は、上記（３）または（４）のポリヌクレオチドのヌクレオチド配列

の全長にわたり９５％同一であり、より好ましくは９７％同一であり、最も好ましくは少なくとも９９％同一である。

【００４８】

上記の本発明のＤＮＡは、前述のタンパク質を、組換えＤＮＡ技術を用いて製造するのに用いることができる。本発明のＤＮＡ及びペプチドは、概略以下のようにして得ることができる。

（Ａ）本発明のタンパク質をコードするＤＮＡをクローニングする。

（Ｂ）タンパク質の全コード領域あるいはその一部をコードするＤＮＡを発現用ベクターに組み込んで、組換えベクターを構築する。

（Ｃ）構築した組換えベクターにより、宿主細胞を形質転換する。

（Ｄ）得られた細胞を培養し、該タンパク質、またはその類縁体を発現させ、カラムクロマトグラフィーにより精製する。

【００４９】

上記の工程中でＤＮＡ、組換え体宿主としての大腸菌等の取り扱いに必要な一般的な操作は、当業者間で通常行われているものであり、たとえば、上記Ｔ．Ｍａｎｉａｔｉｓらの実験操作書に従えば容易に実施できる。使用する酵素、試薬類も全て市販の製品を用いることができ、特に断らない限り、製品で指定されている使用条件に従えば、完全にそれらの目的を達成することができる。以下に上記（Ａ）〜（Ｄ）の工程について更に詳しく説明する。

【００５０】

上記（Ａ）における本発明のタンパク質をコードするＤＮＡのクローニングの手段としては、本願明細書実施例に記載した方法の他に、本発明のヌクレオチド配列（たとえば配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４

８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６
５、１６７、１６９、１７１、１７３、１７５または１７７）の一部を有する合
成ＤＮＡをプライマーとしたＰＣＲ法によって増幅する方法、あるいは、適当な
ベクターに組み込んだＤＮＡを本発明のタンパク質の一部あるいは全領域をコー
ドするＤＮＡ断片もしくは合成ＤＮＡを標識したものとのハイブリダイゼーショ
ンによって選別すること、などが挙げられる。細胞、組織より全ＲＮＡまたはｍ
ＲＮＡ画分を調製したものを用いて直接Ｒｅｖｅｒｓｅ　Ｔｒａｎｓｃｒｉｐｔ
ａｓｅ　Ｐｏｌｙｍｅｒａｓｅ　Ｃｈａｉｎ　Ｒｅａｃｔｉｏｎ（ＲＴ－ＰＣＲ
法）によって増幅することもできる。適当なベクターに組み込んだＤＮＡとして
は、たとえば市販されている（ＣＬＯＮＴＥＣＨ社、ＳＴＲＡＴＡＧＥＮＥ社）
ライブラリーを使用することができる。ハイブリダイゼーションの方法は、当業
者間で通常行われているものであり、たとえば、上記Ｔ．Ｍａｎｉａｔｉｓらの
実験操作書に従えば容易に実施できる。クローン化された本発明のタンパク質を
コードするＤＮＡは目的によりそのまま、または所望により制限酵素で消化した
り、リンカーを付加したりして使用することができる。上記のようにして得られ
るＤＮＡは、配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、
２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、
４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、
７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、
９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２
、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０
、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８
、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５
、１６７、１６９、１７１、１７３、１７５または１７７に記載のヌクレオチド
配列を有する遺伝子であるか、あるいは前述の（３）〜（６）のポリヌクレオチ
ドであればよい。上記（Ｂ）において発現ベクターに組み込むＤＮＡは、上述の
タンパク質の全長をコードする全長ｃＤＮＡでも、ＤＮＡ断片でも良いし、その
一部分を発現する様に構築されたＤＮＡ断片でも良い。

　すなわち、本発明は、上記のＤＮＡを含有する組換えベクターである。

【００５１】

本発明のタンパク質の発現ベクターは、たとえば、本発明のタンパク質をコードするＤＮＡから目的とするＤＮＡ断片を切り出し、該ＤＮＡ断片を適当な発現ベクター中のプロモーターの下流に連結することにより製造することができる。

【００５２】

用いる発現ベクターとしては、複製可能であれば、大腸菌をはじめとする原核生物由来、酵母由来、真菌由来、昆虫ウイルス由来、脊椎動物ウイルス由来いずれのベクターでも良いが、宿主として使用する微生物または細胞に適したものを選択する必要がある。また、発現物に応じて、宿主細胞－発現ベクター系としては、適切な組み合わせが選択される。

微生物を宿主として使用する場合、これら微生物に適したプラスミドベクターが組み換え体ＤＮＡの複製可能な発現ベクターとして一般に用いられる。

【００５３】

たとえば、大腸菌を形質転換するためのプラスミドベクターとしては、プラスミドｐＢＲ３２２やｐＢＲ３２７などを用いることができる。プラスミドベクターは通常複製起源、プロモーター、及び組換え体ＤＮＡで形質転換した細胞を選別するのに有用な表現型を組換え体ＤＮＡに与えるマーカー遺伝子等を含んでいる。プロモーターの例としては、β－ラクタマーゼプロモータ、ラクトースプロモーター、トリプトファンプロモーター等が挙げられる。マーカー遺伝子の例としては、アンピシリン耐性遺伝子やテトラサイクリン遺伝子などが挙げられる。適した発現ベクターの例としては、プラスミドｐＢＲ３２２、ｐＢＲ３２７の他に、ｐＵＣ１８、ｐＵＣ１９等が挙げられる。

【００５４】

酵母で本発明のＤＮＡを発現するためには、複製可能なベクターとして、たとえばＹＥｐ２４を用いることができる。プラスミドＹＥｐ２４はＵＲＡ３遺伝子を含有しており、このＵＲＡ３遺伝子をマーカー遺伝子として利用することができる。酵母細胞用の発現ベクターのプロモーターの例としては、３－ホスホグリセレートキナーゼ、グリセルアルデヒド－３－ホスフェートデヒドロゲナーゼ、アルコールデヒドロゲナーゼなどの遺伝子のプロモーター等が挙げられる。

【００５５】

　真菌で本発明のＤＮＡを発現するための発現ベクターに用いられるプロモーター及びターミネーターの例としては、ホスホグリセレートキナーゼ（ＰＧＫ）、グリセルアルデヒド－３－ホスフェートデヒドロゲナーゼ（ＧＡＰＤ）、アクチン等の遺伝子プロモーター及びターミネーターが挙げられる。適した発現ベクターの例としては、プラスミドｐＰＧＡＣＹ２、ｐＢＳＦＡＨＹ８３等が挙げられる。

【００５６】

　昆虫細胞で本発明のＤＮＡを発現させるための発現ベクターに用いられるプロモーターの例としては、ポリヘドリンプロモーター、Ｐ１０プロモーターなどが挙げられる。

【００５７】

　動物細胞で本発明のＤＮＡを発現させるための組換えベクターは、一般に遺伝子を制御するための機能配列、たとえば、複製起源、本発明のＤＮＡの上流に位置すべきプロモーター、リボソーム結合部位、ポリアデニル化部位や転写終止配列を含有している。本発明のＤＮＡを真核細胞内で発現させるのに用いることができるそのような機能配列はウイルスやウイルス性物質から得ることができる。例えば、ＳＲαプロモーター、ＳＶ４０プロモーター、ＬＴＲプロモーター、ＣＭＶ（サイトメガロウイルス）プロモーター、ＨＳＶ-ＴＫプロモーターなどがあげられる。これらのうち、ＣＭＶプロモーター、ＳＲαプロモーターなどを用いるのが好ましい。また、本発明のタンパク質をコードする遺伝子の上流位置に本来存在するプロモーターも、上述の宿主－ベクター系で使用するのに適しているならば使用することができる。複製起源については、外来性の起源、たとえばアデノウイルス、ポリオーマ、ＳＶ４０等のウイルス由来の複製起点を用いることができる。また、発現ベクターとして宿主染色体に組み込まれるような性質を有するベクターを用いる場合、宿主染色体の複製起源を利用することができる。適した発現ベクターの例としては、プラスミドｐＳＶ－ｄｈｆｒ（ＡＴＣＣ　３７１４６）、ｐＢＰＶ－１（９－１）（ＡＴＣＣ　３７１１１）、ｐｃＤＮＡ３．１（ＩＮＶＩＴＲＯＧＥＮ社）、ｐＭＥ１８Ｓ－ＦＬ３等が挙げられる。

【００５８】

　本発明は、上記の組換えベクターを含む形質転換された細胞である。本発明の複製可能な組換えベクターで形質転換された微生物または細胞は、前述の通り、組換えベクターに与えられた少なくとも１種の表現型によって形質転換されずに残った親細胞から選別される。表現型は少なくとも１種のマーカー遺伝子を組換えベクターに挿入することによって与えることができる。また複製可能なベクターが本来有しているマーカー遺伝子を利用することもできる。マーカー遺伝子の例としては、たとえば、ネオマイシン耐性などの薬剤耐性遺伝子やジヒドロ葉酸レダクターゼをコードする遺伝子などが挙げられる。

【００５９】

　上記（Ｃ）において用いる宿主としては、大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良いが、用いる発現ベクターに適したものを選択する必要がある。微生物の例としては、エシュリヒア　コリ（Ｅｓｃｈｅｒｉｃｈｉａ　ｃｏｌｉ）の菌株、たとえばＥ．ｃｏｌｉ　Ｋ１２株２９４（ＡＴＣＣ　３１４４６）、Ｅ．ｃｏｌｉ　Ｘ１７７６（ＡＴＣＣ　３１５３７）、Ｅ．ｃｏｌｉ　Ｃ６００、Ｅ．ｃｏｌｉ　ＪＭ１０９、Ｅ．ｃｏｌｉ　Ｂ株、あるいはバチラス　サブチリス（Ｂａｃｉｌｌｕｓ　ｓｕｂｔｉｌｉｓ）の如きＢａｃｉｌｌｕｓ属の菌株、あるいはサルモネラ　チフィムリウム（Ｓａｌｍｏｎｅｌｌａ　ｔｙｐｈｉｍｕｒｉｕｍ）またはセラチア　マーゼサンス（Ｓｅｒｒａｔｉａ　ｍａｒｃｅｓａｎｓ）等の大腸菌以外の腸内菌、あるいはシュードモナス（Ｐｓｅｕｄｏｍｏｎａｓ）属の種々の菌株が挙げられる。酵母としては、たとえば、サッカロミセス　セレビシエ（Ｓａｃｃｈａｒｏｍｙｃｅｓ　ｃｅｒｅｖｉｓｉａｅ）、シゾサッカロマイセス　ポンベ（Ｓｃｈｉｚｏｓａｃｃｈａｒｏｍｙｃｅｓ　ｐｏｍｂｅ）、ピキア　パストリス（Ｐｉｃｈｉａ　ｐａｓｔｏｒｉｓ）などが用いられる。真菌としては、たとえば、アスペルギルス　ニドランス（Ａｓｐｅｒｇｉｌｌｕｓ　ｎｉｄｕｌａｎｓ）、アクレモニウム　クリソゲナム（Ａｃｒｅｍｏｎｉｕｍ　ｃｈｒｙｓｏｇｅｎｕｍ）（ＡＴＣＣ　１１５５０）等が挙げられる。

【００６０】

昆虫細胞としては、たとえば、ウイルスがＡｃＮＰＶの場合は、夜盗蛾の幼虫由来株化細胞（Ｓｐｏｄｏｐｔｅｒａ　ｆｒｕｇｉｐｅｒｄａ：Ｓｆ細胞）、Ｔｒｉｃｈｏｐｌｕｓｉａ　ｎｉの卵由来のＨｉｇｈ　ＦｉｖｅＴＭ細胞、などが用いられる。動物細胞の例としては、ＨＥＫ２９３細胞、ＣＯＳ－１細胞、ＣＯＳ－７細胞、Ｈｅｌａ細胞、チャイニーズハムスター（ＣＨＯ）細胞等が挙げられる。これらの中でも、ＣＨＯ細胞およびＨＥＫ２９３細胞が好ましい。細胞を宿主とする場合、用いられる発現ベクターと宿主細胞の組合せは実験の目的により異なるが、その組合せにより、一過的発現、構成的発現の２種類の発現方式が考えられる。

【００６１】

上記（Ｃ）における微生物及び細胞の形質転換とは、ＤＮＡを強制的方法や、細胞の貪食能により微生物や細胞に取り込ませ、プラスミド状態あるいは染色体に組み込まれた状態でＤＮＡの形質を一過的あるいは構成的に発現させることである。当業者であれば公知の方法によって形質転換できる（たとえば実験医学別冊遺伝子工学ハンドブック）。たとえば動物細胞の場合、ＤＥＡＥ－デキストラン法、リン酸カルシウム法、エレクトロポレーション法（電気穿孔法）、リポフェクション法などの方法でＤＮＡを細胞に導入することができる。動物細胞を用いて、本発明のタンパク質を安定に発現させる方法としては、上記の動物細胞に導入された発現ベクターが染色体に組み込まれた細胞をクローン選択によって選択する方法がある。具体的には、上記の選択マーカーを指標にして形質転換体を選択する。さらに、このように選択マーカーを用いて得られた動物細胞に対して、繰り返しクローン選択を行なうことにより本発明のタンパク質の高発現能を有する安定な動物細胞株を得ることができる。また、Ｄｉｈｙｄｒｏｆｏｒａｔｅ　ｒｅｄｕｃｔａｓｅ（ＤＨＦＲ）遺伝子を選択マーカーとして用いた場合Ｍｅｔｈｏｔｒｅｘａｔｅ（ＭＴＸ）濃度を徐々に上げて培養し、耐性株を選択することにより、ＤＨＦＲ遺伝子とともに、本発明のタンパク質をコードするＤＮＡを細胞内で増幅させて、さらに高発現の動物細胞株を得ることもできる。

【００６２】

上記の形質転換された細胞を本発明のタンパク質をコードするＤＮＡが発現可

能な条件下で培養し、本発明のタンパク質を生成、蓄積せしめることによって、本発明のタンパク質を製造することができる。すなわち、本発明は、上記（３）〜（６）に記載の単離されたポリヌクレオチドを含む形質転換された細胞を、該ポリヌクレオチドによりコードされているタンパク質を発現させる条件下培養し、次いで培地から該タンパク質を回収することを含む該タンパク質の製造方法である。

【００６３】

上記の形質転換された細胞の培養は、当業者に公知の方法で行なうことができる（たとえばバイオマニュアルシリーズ４、羊土社）。たとえば動物細胞の場合、各種の動物細胞培養法、たとえば、シャーレ培養、マルチトレー式培養、モジュール培養などの付着培養、または細胞培養用担体（マイクロキャリアー）に付着させるか生産細胞自体を浮遊化させ浮遊培養等の公知の方法により培養を行なえば良い。培地は通常良く用いられる動物細胞用の培地、たとえばＤ−ＭＥＭやＲＰＭＩ１６４０等を用いれば良い。

【００６４】

上記培養物から本発明のタンパク質を分離精製するには、自体公知の分離・精製法を適切に組み合わせて行なうことができる。これらの公知の分離、精製法としては、塩析や溶媒沈澱法などの溶解度を利用する方法、イオン交換クロマトグラフィーなどの荷電の差を利用する方法、透析法、限外ろ過法、ゲルろ過法、およびＳＤＳ−ポリアクリルアミドゲル電気泳動法などの主として分子量の差を利用する方法、アフィニティークロマトグラフィーなどの特異的親和性を利用する方法、逆相高速液体クロマトグラフィーなどの疎水性の差を利用する方法、等電点電気泳動法などの等電点の差を利用する方法などが用いられる。たとえば、本発明のタンパク質は、硫安またはエタノール沈殿、酸抽出、アニオンまたはカチオン交換クロマトグラフィー、ホスフォセルロースクロマトグラフィー、疎水性相互作用クロマトグラフィー、アフィニティクロマトグラフィー、ヒドロキシアパタイトクロマトグラフィーおよびレクチンクロマトグラフィーを含む既知の方法により組換え細胞培養物から回収し、精製することができる。最も好ましくは、高性能液体クロマトグラフィーが精製に使用される。ポリペプチドが細胞内合

成、単離または精製の間に変性するときには、活性なコンフォーメションを再生するためにタンパク質をリフォールディングするためのよく知られた技術を使用できる。

【００６５】

本発明のタンパク質を他のタンパク質との融合タンパク質として製造することができる。これらも、本発明に含まれる。この融合タンパク質を発現する際に用いられるベクターとしては、該タンパク質をコードするＤＮＡを組み込むことができ、かつ該融合タンパク質を発現することができるベクターであれば、いかなるベクターでも用いることができる。本発明のペプチドに融合できるタンパク質としては、たとえばグルタチオン－Ｓ－トランスフェラーゼ（ＧＳＴ）、ヒスチジン残基の６個の連続配列（６×Ｈｉｓ）等が挙げられる。本発明のタンパク質を他の蛋白質と融合した蛋白質として発現させた場合には、融合した蛋白質に親和性をもつ物質を用いたアフィニティークロマトグラフィーを用いて精製することができ、有利である。例えば、ＧＳＴとの融合蛋白質として生産した場合は、グルタチオンをリガンドとするアフィニティークロマトグラフィーにより精製することができる。

【００６６】

本発明は、上記（７）のタンパク質の活性を阻害するタンパク質を含む。たとえば、抗体や上記（７）のタンパク質の活性中心等に結合し、活性の発現を妨げる他のタンパク質が挙げられる。

本発明は、前記の本発明のタンパク質あるいはその部分ペプチドに特異的に結合する抗体ならびにそのような抗体の製造方法に関する。抗体は、本発明のタンパク質を認識し得る抗体であれば、ポリクローナル抗体、モノクローナル抗体、ならびにこれらの抗体のフラグメント、一本鎖抗体、ヒト化抗体の何れであってもよい。抗体フラグメントは、公知の技術によって作製することができる。たとえば、該抗体フラグメントには、限定されるものではないが、Ｆ（ａｂ’）２フラグメント、Ｆａｂ’フラグメント、Ｆａｂフラグメント及びＦｖフラグメントが含まれる。たとえば、モノクローナル抗体またはポリクローナル抗体は、上記（１）または（２）に記載のタンパク質を抗原またはエピトープ含有フラグメン

トとして非ヒト動物に投与することにより得られる。本発明のタンパク質に対する抗体は、本発明のタンパク質あるいはそのペプチドを抗原として用い、自体公知の抗体または抗血清の製造法に従って製造することができる。たとえば実験医学別冊　新遺伝子工学ハンドブック　改訂第３版に記載の方法が挙げられる。

【００６７】

ポリクローナル抗体の場合であれば、たとえば、本発明のタンパク質をウサギなどの動物に本発明のタンパク質あるいはペプチドを注射することにより該タンパク質あるいはペプチドに対する抗体を産生させ、次いで血液を採取し、これを、たとえば硫安沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

【００６８】

モノクローナル抗体の場合は、たとえば、本発明のタンパク質をマウスなどの動物に免疫し、同マウスから脾臓を抽出し、これをすりつぶして細胞にし、マウスミエローマ細胞とポリエチレングリコールなどの試薬により融合させ、これによりできた融合細胞（ハイブリドーマ）の中から、本発明のタンパク質に対する抗体を産生するクローンを選択する。次いで、得られたハイブリドーマをマウス腹腔内に移植し、同マウス内より腹水を回収し、得られたモノクローナル抗体を、たとえば硫安沈殿、イオン交換クロマトグラフィー、あるいは該タンパク質を固定化したアフィニティーカラム等によって精製することで調製することができる。

【００６９】

得られた抗体をヒトに投与する目的で使用する場合は、免疫原性を低下させるために、ヒト型化抗体あるいはヒト抗体を用いることが好ましい。ヒト型化抗体は、トランスジェニックマウスまたは他の哺乳動物を用いて作製することができる。これらのヒト型化抗体のやヒト抗体の一般的概説は、たとえば、Ｍｏｒｒｉｓｏｎ，Ｓ．Ｌ．ｅｔ　ａｌ．〔Ｐｒｏｃ．Ｎａｔｌ．Ａｃａｄ．Ｓｃｉ．ＵＳＡ，８１：６８５１−６８５５（１９８４）〕、Ｊｏｎｅｓ，Ｐ．Ｔ．ｅｔ　ａｌ〔Ｎａｔｕｒｅ　３２１：５２２−５２５（１９８６）〕、野口浩〔医学のあ

ゆみ　１６７：４５７－４６２（１９９３）〕、松本隆志〔化学と生物　３６：４４８－４５６（１９９８）〕によって供されている。ヒト化キメラ抗体は、マウス抗体のＶ領域とヒト抗体のＣ領域を遺伝子組換えにより結合し、作製することができる。ヒト化抗体は、マウスのモノクローナル抗体から相補性決定部位（ＣＤＲ）以外の領域をヒト抗体由来の配列に置換することによって作製できる。また、免疫系をヒトのものと入れ換えたマウスを用いて、該マウスを免疫して、通常のモノクローナル抗体と同様に直接ヒト抗体を作製することもできる。これらの抗体は、タンパク質を発現するクローンを単離したり同定するのに使用できる。また、これらの抗体は、本発明のタンパク質を細胞抽出液、または本発明のタンパク質を産生する形質転換細胞から精製するのに使用できる。更にこれらの抗体は、細胞や組織中の本発明のタンパク質を検出するＥＬＩＳＡやＲＩＡ（ラジオイムノアッセイ）、またはウエスタンブロット系の構築に使用できる。このような検出系は、動物、好ましくは、ヒトの組織または血管内流体などの身体サンプル中に存在する本発明のタンパク質の存在量を検出する診断目的に使用することができる。たとえば、これらの抗体は、炎症、自己免疫疾患、感染症（一例としてＨＩＶ感染）、癌などの、本発明のタンパク質の(発現)異常に起因するＨＦ－κＢの望ましくない活性化によって特徴付けられる疾患の診断に使用できる。疾患の診断の基礎を提供するために、本発明のタンパク質の発現についての通常の値、すなわち標準値が確立されなければならないが、これは当業者においては周知の技術である。すなわち、複合体形成のための適切な条件下で、ヒトあるいは動物のどちらでもよいが、正常の被験者から得られた体液あるいは細胞抽出物と、本発明のタンパク質に対する抗体とを結合させ、この抗体－タンパク複合体の量を化学的または物理的手段により検出し、これを既知量の抗原（本発明のタンパク質）を含む標準液を用いて作成した標準曲線を用いて、正常サンプルから得られた標準値を算出する。標準値と本発明のタンパク質が関係する疾患を潜在的に患う被験者からのサンプルから得られた値と比較し、標準値との偏差によって疾病の存在を確認することができる。また、これらの抗体は、本発明のタンパク質の機能を研究する試薬としても用いることができる。

【００７０】

　本発明の抗体は精製され得、次いで、たとえば、炎症、自己免疫疾患、感染症（一例としてＨＩＶ感染）、癌などの、本発明のタンパク質の（発現）異常に起因するＨＦ－κＢの望ましくない活性化によって特徴付けられる疾患の患者に投与され得る。すなわち本発明は、上記に記載の抗体を有効成分として含有する医薬、および抗体を用いた治療方法である。これらの医薬は治療的使用のためにさらなる有効成分または不活性成分（たとえば、従来の薬学的に受容可能なキャリアまたは希釈剤（たとえば、免疫原性アジュバント）と、生理学的に無毒の安定化剤および賦形剤とともに組み合わされ得る。これらの組み合わせは、濾過滅菌され、そして凍結乾燥により投薬バイアル中に、または安定化水性調製物中の貯蔵物として投薬形態にされ得る。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射などの当業者に公知の方法により行い得る。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。これらの抗体は、本発明のタンパク質で仲介されるＮＦ－κＢの活性化を阻害し、治療効果を示す。

【００７１】

　本発明のＤＮＡは、細胞内シグナリングプロセスに関与する他のタンパク質を単離、同定、クローン化することにも使用できる。たとえば、本発明のタンパク質をコードするＤＮＡ配列は、コードされたタンパク質を「バイト（ｂａｉｔ）」として用いて、ｃＤＮＡまたはゲノムＤＮＡライブラリーから、本発明のタンパク質に結合できるタンパク質をコードする他の配列「プレイ（ｐｒｅｙ）」を単離し、クローン化する酵母ツーハイブリッドシステム（たとえばＮａｔｕｒｅ、３４０：２４５－２４６（１９８９））に用いることができる。同様の方式で、本発明のタンパク質が、他の細胞タンパク質（たとえばＮＩＫ，ＴＲＡＦ２）に結合できるかどうかも決定することができる。あるいは別の方法として、本発明のタンパク質の抗体を用いた免疫沈降法（たとえば、実験医学別冊新遺伝子工学ハンドブック）によって、本発明のタンパク質に結合し得るタンパク質を細胞抽出物から単離する方法が挙げられる。さらに別の方法として、上記に記載のように、本発明のタンパク質を他のタンパク質との融合タンパク質として発現させ、融合タンパク質に対する抗体を用いて免疫沈降法を行ない、本発明のタンパク

質に結合し得るタンパク質を単離する方法が挙げられる。

【００７２】

　診断アッセイは、前述の方法により、ＮＦ－κＢを活性化する機能を持つ（１
）、（２）または（７）のタンパク質遺伝子中の変異を検出することにより疾患
の診断や該疾患への感受性を決定するための方法を提供する。さらに、このよう
な疾患は、個体に由来するサンプル中のタンパク質またはmRNAレベルの異常
な減少または増加を測定することを含む方法によって診断してもよい。発現の減
少または増加は、当該技術でRNAレベルでのポリヌクレオチドの定量によく知
られた方法、たとえば、ＲＴ－ＰＣＲなどの核酸増幅法、およびＲＮａｓｅ保護
法、ノーザンブロット法その他のハイブリダイゼーション法などの方法で測定で
きる。宿主に由来するサンプル中のタンパク質レベルの測定に使用され得るアッ
セイ技術は、当業者によく知られている。そのような方法には、ラジオイムノア
ッセイ、競合的結合測定法、ウェスタンブロット分析およびＥＬＩＳＡアッセイ
が含まれる。本発明のＤＮＡは、本発明のタンパク質またはそのペプチドフラグ
メントをコードするＤＮＡまたはmRNAにおける異常を検出するのに使用でき
る。本発明は、個体における上記（１）、（２）または（７）に記載のタンパク
質の発現に関連した疾患または疾患への感受性を診断する方法に関する。該方法
は、タンパク質をコードするポリヌクレオチド配列における変異を、測定するこ
とを含む。

【００７３】

　本発明のＤＮＡは、本発明のＤＮＡを用いることによって、本発明のタンパク
質またはその部分ペプチドをコードするＤＮＡまたはmRNAの異常を検出する
ことができるので、たとえば、該ＤＮＡまたはmRNAの損傷、突然変異あるい
は発現低下や、増加あるいは発現過多などの遺伝子診断に有用である。すなわち
本発明は、個体における該タンパク質の発現または活性に関連した、該個体にお
ける疾病または疾病への感受性の診断方法であって、

（ａ）個体のゲノムにおける請求項１または２に記載のタンパク質をコードする
ヌクレオチド配列中の変異の存在または不存在を決定し、および／または

（ｂ）該個体に由来するサンプル中での該タンパク質の発現量を分析する、こと

を含む診断方法であって、発現するタンパク質の量が正常の２倍以上あるいは１
／２以下の場合に病気であると診断する方法に関する。

【００７４】

上記（ａ）により、ＮＦ−κＢを活性化する機能を持つ（１）、（２）または
（７）のタンパク質をコードするヌクレオチド配列に変異がある場合は、該変異
がＮＦ−κＢの活性化に関連した疾病を引き起こす可能性がある。あるいは、（
ｂ）により、被験者における前記（１）、（２）または（７）のタンパク発現量
を測定し正常値を異なる値を示す場合は、ＮＦ−κＢを活性化する作用を持つ本
発明の新規タンパク質の発現量異常がＮＦ−κＢの活性化に関連した疾病の原因
である可能性がある。ここで、（ａ）のＮＦ−κＢを活性化する機能を持つ（１
）、（２）または（７）のタンパク質をコードするヌクレオチド配列の変異の有
無を測定する方法としては、それらのタンパク質遺伝子のヌクレオチド配列の一
部をプライマーとして、ＲＴ−ＰＣＲを行い、その後通常のヌクレオチド配列決
定方法によって配列を決定し、変異の有無を検出できる。あるいは、ＰＣＲ−Ｓ
ＳＣＰ法（Ｇｅｎｏｍｉｃｓ、５：８７４−８７９、１９８９年、実験医学別冊
新遺伝子工学ハンドブック）によっても変異の有無を調べることができる。

【００７５】

また、（ｂ）のタンパク発現量を調べる方法としては、たとえば、前記（１６
）に記載の抗体を利用する方法が挙げられる。ヌクレオチド配列を決定する方法
としては、たとえば、上記（３）〜（６）に記載の遺伝子のヌクレオチド配列の
一部をプライマーとしてＲＴ−ＰＣＲを行ない、その後通常のヌクレオチド配列
決定方法によって配列を決定し変異の有無を検出できる。あるいはＰＣＲ−ＳＳ
ＣＰ法（Ｇｅｎｏｍｉｃｓ，５：８７４−８７９、１９８９年、実験医学別冊新
遺伝子工学ハンドブック）によっても変異の有無を調べることができる。

また、本発明は、本発明のタンパク質によるＮＦ−κＢの活性化を阻害または
促進する化合物のスクリーニング方法に関する。

【００７６】

このスクリーニング方法は、

（ａ）ＮＦ−κＢを活性化する作用を有するタンパク質をコードする遺伝子およ

び検出可能なシグナルを提供し得る成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

（ｃ）該形質転換された細胞と１あるいは複数個の被検化合物とを接触させる工程、

（ｄ）検出可能なシグナルを検出する工程、および

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離または同定し、また該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離または同定する工程、

を含む。

【００７７】

　検出可能なシグナルを提供し得る成分としては、たとえばレポーター遺伝子が挙げられる。レポーター遺伝子は、テストを行なう転写因子の活性化を直接検出するかわりに用いられるもので、調べたい遺伝子のプロモーターをレポーター遺伝子につなぎ、レポーター遺伝子の産物の活性を測定することによってプロモーターの転写活性の解析を行なうものである（バイオマニュアルシリーズ４、羊土社（１９９４））。

【００７８】

　レポーター遺伝子としては、その発現産物の活性または生産量（ｍＲＮＡの生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、β−ガラクトシダーゼ、ルシフェラーゼ等の酵素活性を測定することで利用できる。ＮＦ−κＢの活性化を評価するのに用いるレポータープラスミドとしては、ＮＦ−κＢ認識配列をレポーター遺伝子の上流に組み込んだものであればよく、たとえばｐＮＦ−κＢ−Ｌｕｃ（ＳＴＲＡＴＡＧＥＮＥ社）が利用できる。あるいは、Ｔａｎａｋａ　Ｓ．ｅｔ．ａｌ　Ｊ．Ｖｅｔ．Ｍｅｄ．Ｓｃｉ．Ｖｏｌ．５９（７）、Ｒｏｔｈｅ　Ｍ．ｅｔ．ａｌ．Ｓｃｉｅｎｃｅ　Ｖｏｌ．２６９　ｐ１４２４−１４２７（１９９５）に記載のＮＦ−κＢ依存レポータープラスミドが例示される。

【００７９】

　宿主細胞としては、ＮＦ－κＢの活性化を検出し得る細胞であればよく、好ましくは、哺乳動物細胞であり、たとえば２９３ＥＢＮＡ細胞が好適に用いられる。形質転換及び培養に関しては、上記に記載の通りである。

【００８０】

　ＮＦ－κＢの活性化を阻害または促進する化合物のスクリーニングは、具体的には、たとえば、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することにより、ＮＦ－κＢの活性化を阻害または促進する化合物をスクリーニングすることができる。レポーター活性の測定は、当業者に公知の方法（たとえばバイオマニュアルシリーズ４、羊土社（１９９４））で行なうことができる。スクリーニングの被検物質には特に制限はなく、低分子化合物、ペプチドなどが挙げられる。被検化合物は、人工的に合成したものであっても、天然に存在するものであっても良い。また単一物質でも、混合物でもい。検出可能なシグナルとしては、上記レポーター遺伝子の他に、ＮＦ－κＢの活性化によって発現が誘導されることが知られている、たとえばＩＬ－１やＴＮＦ－αの遺伝子のｍＲＮＡ量あるいはタンパク量を測定しても良い。ｍＲＮＡ量の測定は、たとえばノーザンハイブリダイゼーションやＲＴ－ＰＣＲ法などが挙げられる。タンパク量の測定はたとえば抗体を用いる方法が挙げられる。抗体は公知の方法によって作製しても良いし、市販のもの（たとえば和光純薬工業株式会社）を使用することもできる。

【００８１】

　また、以下の（ａ）～（ｆ）の工程により医薬組成物を製造することも可能である。

（ａ）ＮＦ－κＢを活性化する作用を有するタンパク質をコードする遺伝子および検出可能なシグナルを与えることができる成分を細胞に提供する工程、

（ｂ）該遺伝子が形質転換された細胞内で発現可能となる条件下で形質転換された宿主細胞を培養する工程、

（ｃ）該形質転換された宿主細胞と１あるいは複数個の化合物とを接触させる工

程、

（ｄ）検出可能なシグナルを測定する工程、

（ｅ）該検出可能なシグナルを正常より２倍以上に増加させる化合物を活性化剤化合物として単離または同定し、また該検出可能なシグナルを２分の１以下に減少させる化合物を阻害剤化合物として単離または同定する工程、および

（ｆ）単離または同定された化合物を医薬組成物として最適化する工程。

【００８２】

本願発明のタンパク質は、以下の工程により、該タンパク質のアゴニスト、アンタゴニストまたは阻害剤を、構造を基礎にして設計する方法に使用してもよい。

（ａ）まず、タンパク質の三次元構造を決定する工程、

（ｂ）アゴニスト、アンタゴニストまたは阻害剤の反応性部位または結合部位と思われる部位の三次元構造を推論する工程、

（ｃ）推論した結合部位または反応性部位に結合するかあるいは結合すると予測される候補化合物を合成する工程、および

（ｄ）該候補化合物が本当にアゴニスト、アンタゴニストまたは阻害剤であるか否かを試験する工程。

【００８３】

また本発明は、上記スクリーニングによって得られた化合物を含む。しかしながら、本発明のスクリーニング方法は、上記の方法に限定されるものではない。さらに、上記（１４）に記載の方法により医薬組成物を製造する方法も含む。

【０８４】

該候補化合物には特に制限はなく、低分子化合物、ペプチドなどが挙げられ、また、人工的に合成したものであっても、天然に存在するものであっても良い。上記スクリーニングによって得られた化合物は、ＮＦ－κＢの活性化を阻害または促進する作用を有しているので、ＮＦ－κＢの望ましくない活性化あるいは不活性化に起因する疾患を治療または予防するための医薬として有用である。混合物から目的化合物を単離、精製するには、自体公知の方法、例えば濾過、抽出、洗浄、乾燥、濃縮、結晶化、各種クロマトグラフィー等を適宜組み合わせて行な

うことができる。化合物の塩を取得したい時は、化合物が塩の形で得られる場合にはそのまま精製すれば良く、また遊離の形で得られる場合には、通常の方法により適当な溶媒に溶解または懸濁し、所望の酸または塩基を添加し、塩を形成させて単離精製すれば良い。本発明の方法を用いて得られる化合物またはその塩を医薬組成物とする場合、常法により製剤化することができる。すなわち活性成分として有効な量の上記化合物またはその薬理的に許容される塩と、薬理的に許容される担体とを混合すれば良い。製剤化は選訳された投与様式に適した形態が選ばれる。経口投与に適した組成物としては、錠剤、顆粒剤、カプセル剤、丸剤、および散剤などの固体形態、溶液剤、シロップ剤、エリキシル剤、および懸濁液剤などの液体形態が挙げられる。非経口投与に有用な形態としては、無菌溶液剤、乳剤、および懸濁液剤が挙げられる。上記の担体としては、例えばゼラチン、乳糖、グルコース等の糖類、コーン・小麦・米・とうもろこし澱粉等の澱粉類、ステアリン酸等の脂肪酸、ステアリン酸カルシウム・ステアリン酸マグネシウム等の脂肪酸塩、タルク、植物油、ステアリンアルコール・ベンジルアルコール等のアルコール、ガム、ポリアルキレングリコール等が挙げられる。これらのうち液状担体の例としては、一般に水、生理食塩水、デキストロースまたは類似の糖溶液、エチレングリコール、プロピレングリコール、ポリエチレングリコール等のグリコール類が挙げられる。

【００８５】

本発明は、ＮＦ−κＢの活性化阻害剤または活性化剤としての活性について化合物をスクリーニングするためのキットである。該キットは、

（ａ）ＮＦ−κＢを活性化する作用を有するタンパク質をコードする遺伝子およびＮＦ−κＢの活性化後、その活性化が検出可能なシグナルを提供する成分を含有する細胞、

（ｂ）該検出可能なシグナルを測定するための試薬、から成り、ＮＦ−κＢの活性化を阻害または促進する化合物をスクリーニングするために必要な試薬類を含む。

【００８６】

別の側面において、本発明は、

（ａ）配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２、２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるヌクレオチド配列を有する本発明のポリヌクレオチド；

（ｂ）（ａ）のヌクレオチド配列に相補的なヌクレオチド配列；

（ｃ）配列番号１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６または１７８で表されるアミノ酸配列を有する本発明のタンパク質またはそれらの断片；または

（ｄ）（ｃ）の本発明のタンパク質に対する抗体；を含む診断キットに関する。

【０○８７】

　少なくとも（ａ）～（ｄ）のいずれかを含むキットは、炎症、自己免疫疾患、感染性疾患（たとえばＨＩＶ感染）および癌などの疾患または該疾患への感受性を診断するのに有用である。

【０○８８】

　ＮＦ－κＢは、炎症、自己免疫疾患、ガン及びウイルス感染などの多種の病理

学的状態におけるその関与のため、薬物デザイン及び治療介在のための魅力的な標的である。多数の実験が、ＮＦ－κＢ活性の阻害が深い生理学的作用を有し得ることを示している（たとえば、Ann. Rheum. Dis. 57, 738-741 (1998), American Journal of Pathology 152, 793-803 (1998), ARTHRITIS & RHEUMATISM 40, 226-236 (1997), Am. J. Respir. Crit. Care Med. 158, 1585-1592 (1998), J. Exp. Med. 188 1739-1750 (1998), Gut 42, 477-484 (1998), The Journal of Immunology 161, 4572-4582 (1998), Nature Medicine 3,894-899 (1997)）。本明細書中に報告するＮＦ－κＢを活性化する作用を有する新規タンパク質の発見により、異常なＮＦ－κＢ機能を阻害する新しい方法が提供された。さらなる具体例において、本発明は、ＮＦ－κＢの活性化を阻害するための前記のＮＦ－κＢを活性化する作用を有するタンパク質の機能を阻害する化合物を用いる方法に関する。上記スクリーニング方法によって得られた、ＮＦ－κＢの活性化を阻害する化合物は、たとえば炎症、自己免疫疾患、感染症（１例としてＨＩＶ感染症）、ガンなどの、ＮＦ－κＢの望ましくない活性化によって特徴つけられる疾患の治療または予防する医薬として有用である。更に、ＮＦ－κＢの活性化が細胞のアポトーシスを阻害することが、最近明らかになりつつある。上記スクリーニング方法によって得られた、ＮＦ－κＢの活性化を阻害する化合物は、アポトーシスを促進する機能を持つ可能性も考えられる。アポトーシスの誘導が治療につながる疾患としては、腫瘍が挙げられる。

【００８９】

逆に、アポトーシスの抑制が治療につながる疾患としてはＧＶＨＤ、Ｔｏｘｉｃ　ｅｐｉｄｅｒｍａｌ　ｎｅｃｒｏｌｙｓｉｓ（ＴＥＮ）などの皮膚疾患、増殖性腎炎（ＩｇＡ腎炎、紫斑病性腎炎、ループス腎炎）、劇症肝炎などが挙げられる。よって、上記スクリーニング方法によって得られた、ＮＦ－κＢの活性化を促進する化合物はこれらの疾患の治療または予防のための医薬として有用である。

【００９０】

更に、本発明のタンパク質をコードする遺伝子は、癌、自己免疫疾患、アレルギー性疾患、および炎症性応答を初めとする様々な疾患の治療を目的とした遺伝

子治療にも有用である。遺伝子治療とは、疾病の治療を目的として、遺伝子または遺伝子を導入した細胞をヒトの体内に投与することを意味する。本発明のタンパク質や該タンパク質をコードするDNAは、診断目的にも使用できる。

【００９１】

　本発明のスクリーニング方法を用いて得られる化合物またはその塩を上述の医薬組成物として使用する場合、常套手段に従って実施することができる。たとえば、錠剤、カプセル剤、エリキシル剤、マイクロカプセル剤、無菌性溶液、懸濁液剤などとすることができる。このようにして得られる製剤は安全で低毒性であるので、たとえば、ヒトや哺乳動物（たとえば、ラット、ウサギ、ヒツジ、ブタ、ウシ、ネコ、イヌ、サルなど）に対して投与することができる。患者への投与は、たとえば、動脈内注射、静脈内注射、皮下注射など当業者に公知の方法により行いうる。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。また、該化合物がDNAによりコードされうるものであれば、該DNAを遺伝子治療用ベクターに組込み、遺伝子治療を行うことも考えられる。投与量、投与方法は、患者の体重や年齢、症状などにより変動するが、当業者であれば適宜選択することが可能である。すなわち本発明は、上記化合物を有効成分として含有する医薬に関する。

【００９２】

　さらに、上記化合物は、炎症、自己免疫疾患、ウイルス性疾患、感染症、ガンなどの、ＮＦ－κＢの望ましくない活性化によって特徴つけられる疾患の治療または予防する医薬として有用である。すなわち本発明は、上記化合物を含む炎症、自己免疫疾患、ウイルス性疾患、ガンなどの医薬に関する。具体的には、例えば、慢性関節リウマチ、変形性関節症、全身性エリテマトーデス、糖尿病、敗血症、喘息、アレルギー性鼻炎、虚血性心疾患、炎症性腸疾患、くも膜下出血、ウイルス肝炎、エイズ、などに対する治療及び予防薬として有用である。

【００９３】

　さらにまた、本発明は、炎症、自己免疫疾患、ウイルス性疾患、ガンなどの医薬の製造における上記（１４）記載の方法により製造された医薬組成物の使用も含む。また本発明は、上記（３）～（６）に記載の遺伝子に対するアンチセンス

オリゴヌクレオチドである。アンチセンスオリゴヌクレオチドは、標的とした遺伝子配列に対して相補的な配列を持つオリゴヌクレオチドを用いて、タンパク質への翻訳、細胞質への輸送、あるいは全体的な生物活性機能に必要な他の活性等のＲＮＡの機能を阻害することによって、標的遺伝子の発現を抑制することができる。この際、アンチセンスオリゴヌクレオチドとしては、ＲＮＡを用いても良いし、ＤＮＡを用いても良い。本発明のＤＮＡ配列は、本発明のタンパク質をコードする遺伝子から転写されたｍＲＮＡとハイブリダイズし得るアンチセンスオリゴヌクレオチドを作製するために使用できる。一般にアンチセンスオリゴヌクレオチドが、その遺伝子の発現に対して抑制的に作用することは公知での事実である（たとえば、細胞工学　Ｖｏｌ．１３　Ｎｏ．４（１９９４））。 本発明のタンパク質をコードする遺伝子に対するアンチセンスコード配列を有するオリゴヌクレオチドは、標準の方法で細胞内に導入することができ、該オリゴヌクレオチドは、本発明のタンパク質をコードする遺伝子のｍＲＮＡの翻訳を効果的に遮断して、その発現を遮断して、望ましくない作用が阻害される。

【００９４】

本発明のオリゴヌクレオチドは、天然に見出されるオリゴヌクレオチドの他に、修飾されたものであっても良い〔たとえば、村上＆牧野：細胞工学　Ｖｏｌ．１３　Ｎｏ．４　ｐ２５９−２６６（１９９４）、村上章：蛋白質核酸酵素　Ｖｏｌ．４０　Ｎｏ．１０　ｐ１３６４−１３７０（１９９５）、竹内恒成ら：実験医学　Ｖｏｌ．１４　Ｎｏ．４　ｐ８５−９５（１９９６〕。従って、オリゴヌクレオチドは変化した糖部分あるいは糖間部分を有していても良い。これらの例は、当該技術分野において使用が知られているホスホチオエート及び他のイオウ含有種である。幾つかの好ましい態様に従えば、オリゴヌクレオチドの少なくとも一つのホスホジエステル結合が、その活性が調節されるべきＲＮＡが位置する細胞の領域に浸透する組成物の能力を高める機能を有する構造により置換される。

【００９５】

このような置換は、ホスホロチオエート結合、ホスホロアミデート結合、メチルホスホネート結合または短鎖アルキルもしくはシクロアルキル構造を含むこと

が好ましい。オリゴヌクレオチドはまた、少なくとも幾つかの修飾されたヌクレオチド型を含んでいても良い。従って、天然に通常見いだされるもの以外のプリン及びピリミジンを使用していても良い。同様に本発明の本質的な意図が実行される限り、ヌクレオチドサブユニットのフラノシル部分を修飾することもできる。このような修飾の例は、２'－Ｏ－アルキル－、及び２'－ハロゲン置換ヌクレオチドである。本発明において有用な幾つかの糖部分の２'位の修飾の例は、ＯＨ、ＳＨ、SCH_3、OCH_3、ＯＣＮ、または$O(CH_2)_nCH_3$（ここでｎは１から約１０である）、及び同様の特性を有する他の置換基である。全てのこのような類似体は、本発明の遺伝子のｍＲＮＡとハイブリダイズしてそのＲＮＡの機能を阻害する機能を果たす限り、本発明に包含される。

【００９６】

本発明のオリゴヌクレオチドは、約３から約５０ヌクレオチドを含み、約８から約２５ヌクレオチドを含むことが好ましく、約１２から約２０ヌクレオチドを含むことがさらに好ましい。本発明のオリゴヌクレオチドは、周知の方法である固相合成法により作製することができる。このような合成のための装置は、Ａｐｐｌｉｅｄ　Ｂｉｏｓｙｓｔｅｍｓを含む幾つかの業者により販売されている。ホスホチオエート等の他のオリゴヌクレオチドの製造も当業者に公知の方法で作製できる。

【００９７】

本発明のオリゴヌクレオチドは、本発明の遺伝子から転写されるｍＲＮＡとハイブリダイズできるように設計される。与えられた遺伝子の配列に基づいてアンチセンスオリゴヌクレオチドを設計する方法は、当業者であれば容易である〔たとえば、村上および牧野：細胞工学　Ｖｏｌ．１３　Ｎｏ．４　ｐ２５９－２６６（１９９４）、村上章：蛋白質核酸酵素　Ｖｏｌ．４０　Ｎｏ．１０　ｐ１３６４－１３７０（１９９５）、竹内恒成ら：実験医学　Ｖｏｌ．１４　Ｎｏ．４　ｐ８５－９５（１９９６）〕。　最近の研究は、ｍＲＮＡの５'領域、好ましくは翻訳開始部位を含む領域に設計されたアンチセンスオリゴヌクレオチドが、遺伝子の発現の阻害に最も効果的であることを示唆している。アンチセンスオリゴヌクレオチドの長さは、１５から３０ヌクレオチドが好ましく、２０から２

５ヌクレオチドがより好ましい。ホモロジー検索で他のｍＲＮＡとの相互作用がないこと、オリゴヌクレオチド配列内で二次構造を取らないことを確認しておくことは重要である。設計したアンチセンス分子が機能したかどうかの評価は、適当な細胞を用いて、該細胞にアンチセンスオリゴヌクレオチドを導入し、当業者には公知の方法で、対象ｍＲＮＡの量（たとえば、ノーザンブロットまたはＲＴ−ＰＣＲ法）、あるいは対象タンパク質の量（たとえば、ウエスタンブロットまたは蛍光抗体法）を測定することにより、発現抑制の効果を確認できる。

【００９８】

一方、三重らせん形成（トリプル・ヘリックス技術）は、核内のＤＮＡを標的とした、主に転写の段階での遺伝子発現制御方法である。オリゴヌクレオチドは、主に転写に関与する遺伝子領域に設計され、それにより、転写及び本発明のタンパク質の産生を抑える。これらのＲＮＡ、ＤＮＡ、オリゴヌクレオチドは、公知の合成装置などを用いて製造することができる。

【００９９】

本発明のオリゴヌクレオチドは、標的核酸配列を含む細胞に、たとえばリン酸カルシウム法、リポフェクション法、エレクトロポレーション法、マイクロインジェクション法などのDNAトランスフェクション法、またはウイルスなどの遺伝子導入ベクターの使用を含む遺伝子導入法のいずれを用いて導入してもよい。適切なレトロウイルスベクターを用いてアンチセンスオリゴヌクレオチド発現ベクターを作製し、その後、該発現ベクターを細胞とｉｎ ｖｉｖｏまたはｅｘ ｖｉｖｏで接触させることにより、標的核酸配列を含む細胞に導入できる。

本発明のＤＮＡは、アンチセンスＲＮＡ／ＤＮＡ技術またはトリプル・ヘリックス技術を用いて、本発明のタンパクを介するＮＦ−κＢの活性化を阻害するのに使用できる。

【０１００】

本発明のタンパク質をコードする遺伝子のアンチセンスオリゴヌクレオチドは、たとえば炎症、自己免疫疾患、感染症（たとえば、ＨＩＶ感染症症）、ガンなどの、ＮＦ−κＢの望ましくない活性化によって特徴つけられる疾患を治療または予防する医薬として有用である。すなわち、本発明は、上記アンチセンスオリ

ゴヌクレオチドを有効成分として含有する医薬である。また、本発明のアンチセ
ンスオリゴヌクレオチドは、ノーザンハイブリダイゼーション法またはＰＣＲ法
を用いてそれらの疾病の検出に利用することもできる。

【０１０１】

　本発明は、ＮＦ－κＢの活性化を阻害するリボザイムも含む。リボザイムは、
核酸のヌクレオチド配列を認識して、核酸を切断する活性を持つＲＮＡである（
たとえば、柳川弘志　実験医学バイオサイエンス１２、ＲＮＡのニューエイジ）
。リボザイムは、選択された標的ＲＮＡ、たとえば本発明のタンパク質をコード
するｍＲＮＡを開裂するように製造することができる。本発明のタンパク質をコ
ードするＤＮＡのヌクレオチド配列を基に、本発明のタンパク質のｍＲＮＡを特
異的に切断するリボザイムを設計することができ、かようなリボザイムは本発明
のタンパク質のｍＲＮＡに対して相補的な配列を有し、該ｍＲＮＡと相補的結合
し、ついで該ｍＲＮＡが開裂され本発明のタンパク質の発現が減少し（または完
全に発現せず）、発現減少のレベルは標的細胞内でのリボザイム発現のレベルに
依存している。

【０１０２】

　よく用いられるリボザイムには、ハンマーヘッド型とヘアピン型の２種類があ
り、特にハンマーヘット型リボザイムは切断活性に必要な一次構造や二次構造が
よく調べられており、当業者であれば、本発明のタンパク質をコードするＤＮＡ
のヌクレオチド配列情報のみで容易にリボザイムの設計が可能である〔たとえば
、飯田ら：細胞工学Vol.16 No.3,p438-445（1997）、大川＆平比良：実験医学Vol
.12 No.12 p83-88(1994)〕。ハンマーヘッドリボザイムは、標的ＲＮＡと相補鎖
を形成する２ヶ所の認識部位（認識部位Ｉと認識部位ＩＩ）と活性部位からなる
構造をなし、標的ＲＮＡと認識部位で相補対を形成した後、標的ＲＮＡのＮＵＸ
の配列（Ｎ：ＡまたはＧまたはＣまたはＵ、Ｘ：ＡまたはＣまたはＵ）の３'末
端側で切断することが知られており、特にＧＵＣ（あるいはＧＵＡ）が一番高い
活性を持つことが知られている〔たとえばKoizumi,Mら：Nucl. Acids Res.17,705
9-7071(1989)、飯田ら：細胞工学Vol.16No.3,p438-445（1997）、大川＆平比良：
実験医学Vol.12 No.12 p83-88(1994)、川崎＆多比良：実験医学 Vol.18 No.3 p3

81-386（2000）〕。

【０１０３】

　そこでまず、本発明のＤＮＡ配列の中からＧＴＣ（またはＧＴＡ）の配列を探し出し、その前後で数ヌクレオチドから十数ヌクレオチドの相補対をつくることができるようにリボザイムを設計する。設計したリボザイムの適切性の評価は、たとえば、大川＆平比良の文献〔実験医学Vol.12 No.12 p83-88(1994) 〕に記載の方法によって、作製したリボザイムが、イン　ビトロで標的ｍＲＮＡを切断できるかどうかを調べることで評価できる。リボザイムの調製は、ＲＮＡ分子を合成するのための当分野で周知の方法により調製する。

【０１０４】

　別法としては、リボザイムの配列をＤＮＡ合成機で合成し、たとえばＴ７或いはＳＰ６のような適切なＲＮＡポリメラーゼプロモータを有する多種のベクターに組み込み、イン　ビトロで酵素的にＲＮＡを合成させる方法が挙げられる。これらのリボザイムは、たとえばマイクロインジェクション法などの遺伝子導入方法によって細胞内に導入できる。あるいは別の方法として、リボザイムＤＮＡを適当な発現ベクターに組み込んで、株細胞、細胞或いは組織内に導入する。選択された細胞中にリボザイムを導入するのに、適切なベクターを使用することができ、たとえばプラスミドベクター、動物ウイルス（たとえばレトロウイルス、アデノウイルス、ヘルペスあるいはワクシニアウイルス）ベクターがこれらの目的に通常用いられるこれらのリボザイムは、本発明のタンパク質で仲介されるＮＦ－κＢの活性化を阻害する作用を有する。

【０１０５】

　本発明はまた、機能を有する新規遺伝子の取得方法であり、オリゴキャッピング法を用いて完全長ｃＤＮＡライブラリーを作製する方法および該機能を有するタンパク質の存在を示すシグナル因子を用いる方法からなる取得方法に関する。シグナル因子には、たとえばレポーター遺伝子が挙げられる。

【０１０６】

　機能を有する遺伝子（ｃＤＮＡ）を多数取得するためには、不完全長のものが多いｃＤＮＡライブラリーを用いると効率が悪い。したがって、全体のクローン

の中で、完全長のものの割合が高いライブラリーが必要となる。完全長ｃＤＮＡは遺伝子から出来るｍＲＮＡの完全なコピーのことである。オリゴキャッピング法で作製したｃＤＮＡライブラリーは、完全長ｃＤＮＡの割合が５０～８０％であり、従来の方法で作製されたｃＤＮＡライブラリーと比べて、５～１０倍の完全長ｃＤＮＡクローンの濃縮になっている（菅野純夫：月刊　BIO INDUSTRY Vol.16 No.11 p19-26）。完全長ｃＤＮＡは、遺伝子の機能解析においては、タンパク質発現のために必須なクローンであり、完全長ｃＤＮＡのクローンそのものが活性測定のための材料として極めて重要なものであるため、遺伝子の機能解析を試みるに際して、完全長ｃＤＮＡのクローニングは必須の要件である。さらにその配列を決定することで、それがコードするタンパク質の一次配列を確定するための重要な情報となると同時に、遺伝子の全エクソンの配列も分かる。すなわち、完全長ｃＤＮＡは、遺伝子を同定する上で貴重な情報、たとえばタンパク質の一次配列、エクソン－イントロン構造、ｍＲＮＡの転写開始点、プロモーターの位置などを決めるための情報をも与える。

【０１０７】

オリゴキャッピング法による完全長ｃＤＮＡライブラリー作製は、たとえば実験医学別冊新遺伝子工学ハンドブック改訂第３版（１９９９年）に記載の方法に従い行うことができる。機能を有するタンパク質の存在を示すレポーター遺伝子は、転写因子等のタンパク質因子が結合できる適切な発現制御配列部分（１つまたは複数）と、その転写因子等による活性化を測定できる構造遺伝子部分からなる。構造遺伝子部分は、その発現産物の活性または生産量（ｍＲＮＡの生産量も含まれる）を当業者が測定可能なものであれば、いかなるペプチド、タンパク質をコードする遺伝子も用いることができる。たとえば、クロラムフェニコールアセチルトランスフェラーゼ、β－ガラクトシダーゼ、ルシフェラーゼ等を用いることができ、その酵素活性を測定することで利用できる。

【０１０８】

本発明において、オリゴキャッピング法とは、鈴木・菅野　実験医学別冊　遺伝子工学ハンドブック改訂第３版に記載のように、ＢＡＰ，ＴＡＰ，ＲＮＡリガーゼにより、キャップ構造を合成オリゴに置換する方法である。

【０１０９】

　本発明の方法は、イン　ビトロ（in　vitro）の系、あるいは細胞を用いて（cell－based）の系のどちらの方法でも良く、好ましくは細胞を用いた系である。細胞は、原核大腸菌をはじめとする原核生物、酵母、真菌等の微生物、及び昆虫や動物等の細胞のいずれでも良く、好ましくは動物細胞であり、２９３ＥＢＮＡ細胞、ＮＩＨ３Ｔ３細胞が例示できる。

【０１１０】

　機能を有するタンパク質の存在を示すレポーター遺伝子としては、本願明細書に示したＮＦ－κＢのレポーター遺伝子の他に、たとえばＣＲＥＢ（cAMP responsive element binding protein）結合配列あるいはＡＰ－１（activator protein-1）結合配列をレポーター遺伝子の発現制御配列部分に有するレポーター遺伝子が挙げられる。たとえば、ＣＲＥＢを活性化する機能を有する遺伝子を取得したい場合は、ＣＲＥＢ依存レポータープラスミドとオリゴキャッピング法で作製した完全長ｃＤＮＡクローンを細胞に共導入し、その中からレポーター活性が上昇したプラスミドを選ぶことによって、該目的を達成することができる。また、ＣＲＥＢを抑制する機能を有する遺伝子を取得したい場合は、ＣＲＥＢ依存レポータープラスミドとオリゴキャッピング法で作製した完全長ｃＤＮＡクローンを細胞に共導入し、その中からレポーター活性が減少したプラスミドを選ぶことによって、該目的を達成することができる。この場合、細胞に何らかの刺激を加えた状態で行なっても良い。ｃＤＮＡクローンの細胞への導入は、１クローンでも良いし、複数のクローンを同時に導入しても良い。本発明の該方法の一例は、本願明細書実施例に詳細に記述してある。あるいは、完全長ｃＤＮＡとレポーター遺伝子を細胞に導入した後、細胞をＩＬ－１あるいはＴＮＦ－αなどで刺激し、レポーター活性の上昇の弱いクローンを選ぶことによって、ＮＦ－κＢの活性化を抑制する機能を有する遺伝子を取得するためのスクリーニング系を構築することもできる。

【０１１１】

　しかしながら、本発明の該方法は、この方法に限定されるものではない。また、本発明のｃＤＮＡは、完全長ｃＤＮＡであるため、その５’末端の配列がｍＲ

ＮＡの転写開始点であり、該ｃＤＮＡ配列をゲノムのヌクレオチド配列と比較することにより、該遺伝子のプロモーター領域を同定することに利用できる。ゲノムのヌクレオチド配列は、データベースに公知の配列として登録されている場合はその配列を利用できる。あるいは、該ｃＤＮＡを用いてたとえばハイブリダイゼーションによってゲノムライブラリーからクローニングし、ヌクレオチド配列を決めることもできる。このようにして、本発明のｃＤＮＡのヌクレオチド配列をゲノムの配列と比較することによって、その上流に存在する該遺伝子のプロモーター領域を同定することが可能である。さらに、このようにして同定した該遺伝子のプロモーター断片を用いて該遺伝子の発現を調べるレポータープラスミドを作製することができる。レポータープラスミドは、大方の場合、転写開始点からその上流２ｋｂ、好ましくは転写開始点からその上流１ｋｂのＤＮＡ断片をレポーター遺伝子の上流に組み込むことによって作製できる。さらに該レポータープラスミドは、該遺伝子の発現を増強あるいは減弱させる化合物のスクリーニングに利用できる。具体的には例えば、該レポータープラスミドで適当な細胞を形質転換し、一定時間培養した形質転換細胞に、被験物質を任意の量添加し、一定時間後の該細胞が発現するレポーター活性を測定し、被験物質を添加しない細胞のレポーター活性と比較することによりスクリーニングすることができる。これらも本発明に含まれる。

【０１１２】

また本発明は、配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２，２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１０２、１０４、１０６、１０８、１１０、１１２、１１４、１１６、１１８、１２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１７３、１７５または１７７で表されるヌクレオチド配列のうち少なくとも１以上を含むデータセットおよび／または配列番号

１、３、５、７、９、１１、１３、１５、１７、１９、２１、２３、２５、２７

、２９、３１、３３、３５、３７、３９、４１、４３、４５、４７、４９、５１

、５３、５５、５７、５９、６１、６３、６５、６７、６９、７１、７３、７５

、７７、７９、８１、８３、８５、８７、８９、９１、９３、９５、９７、９９

、１０１、１０３、１０５、１０７、１０９、１１１、１１３、１１５、１１７

、１１９、１２１、１２３、１２５、１２７、１２９、１３１、１３３、１３５

、１３７、１３９、１４１、１４３、１４５、１４７、１４９、１５２、１５４

、１５６、１５８、１６０、１６２、１６４、１６６、１６８、１７０、１７２

、１７４、１７６および１７８で表されるアミノ酸配列のうち少なくとも１以上

を含むデータセットを保存したコンピュータ読み込み可能媒体に関する。

【０１１３】

　さらに本発明は、上記に記載の媒体上のデータと他のヌクレオチド配列のデー

タを比較して相同性の算出を行う方法に関する。すなわち、本発明の遺伝子およ

びアミノ酸配列は、その２次元および３次元構造を決定し、たとえば同様の機能

を有する相同性の高いさらなる配列を同定するための貴重な情報源となる。これ

らの配列をコンピュータ読み込み可能媒体に保存し、ついで既知の高分子構造プ

ログラムにおいて保存したデータを用いて、ＧＣＧのような既知検索ツールを用

いてデータベースを検索すれば、データベース中の、ある相同性を有する配列を

見出すことは容易である。

【０１１４】

　コンピュータ読み取り可能媒体は情報またはデータを保存するのに用いる物体

のいずれの組成物であってもよく、たとえば、市販フッロッピーディスク、テー

プ、チップ、ハードドライブ、コンパクトディスク、およびビデオディスク等が

ある。また、本媒体上のデータは、他のヌクレオチド配列のデータと比較して相

同性の算出を行なう方法を可能にする。この方法には、本発明ポリヌクレオチド

配列を含む第一のポリヌクレオチド配列をコンピュータ読み込み可能媒体中に提

供し、次いで、該第一のポリヌクレオチド配列を少なくとも一つの第二のポリヌ

クレオチドまたはポリペプチド配列と比較して相同性を同定する工程を含む。

【０１１５】

　本発明はまた、配列番号2、4、6、8、10、12、14、16、18、2
0、22、24、26、28、30、32、34、36、38、40、42、4
4、46、48、50、52、54、56、58、60、62、64、66、6
8、70、72、74、76、78、80、82、84、86、88、90、9
2、94、96、98、100、102、104、106、108、110、1
12、114、116、118、120、122、124、126、128、1
30、132、134、136、138、140、142、144、146、1
48、150、151、153、155、157、159、161、163、1
65、167、169、171、173、175または177から選択されるヌ
クレオチド配列の全てまたは一部を含むポリヌクレオチドが固定されている不溶
性基質に関する。ＤＮＡプローブである複数の各種ポリヌクレオチドがスライド
ガラス等の特別に加工された基質上に固定され、次いで標識された標的ポリヌク
レオチドを、固定化されたポリヌクレオチドとハイブリダイズさせ、それぞれの
プローブからのシグナルを検出する。得られるデータは、解析され、遺伝子発現
が測定される。

【０１１６】

　本発明はさらにまた、配列番号1、3、5、7、9、11、13、15、17
、19、21、23、25、27、29、31、33、35、37、39、41
、43、45、47、49、51、53、55、57、59、61、63、65
、67、69、71、73、75、77、79、81、83、85、87、89
、91、93、95、97、99、101、103、105、107、109、
111、113、115、117、119、121、123、125、127、
129、131、133、135、137、139、141、143、145、
147、149、152、154、156、158、160、162、164、
166、168、170、172、174、176または178で表されるアミ
ノ酸配列から選択されるアミノ酸配列の全てまたは一部を含むポリペプチドが固
定されている不溶性基質に関する。このタンパク質を固定した不溶性基質と、生
物由来の細胞抽出液とを混合し、不溶性基質上に捕獲された、診断あるいは新薬
開発のために有効であることが期待されるタンパク質などの細胞由来の成分を、

単離あるいは同定することができる。

【０１１７】

【実施例】

以下に、実施例を挙げて本発明を詳しく説明するが、本発明は、これらの例に何ら限定されるものではない。

【０１１８】

（実施例１）オリゴキャッピング法を用いた完全長ｃＤＮＡライブラリーの作製

（１）ヒト肺線維芽細胞（Ｃｒｙｏ　ＮＨＬＦ）からのＲＮＡ調製

ヒト肺線維芽細胞（Ｃｒｙｏ　ＮＨＬＦ：三光純薬株式会社より購入）を、添付のプロトコールに従って培養した。１０ｃｍシャーレ５０枚まで継代培養した後、セルスクレーパーで細胞を回収した。次いで、回収した細胞からＲＮＡ抽出用試薬ＩＳＯＧＥＮ（ニッポンジーンより購入）を用いて全ＲＮＡを取得した。取得の具体的方法は、試薬のプロトコールに従った。次いで、オリゴ－ｄＴ　セルロース　カラムを用いて、全ＲＮＡからポリＡ＋ＲＮＡを取得した。ポリＡ＋ＲＮＡ取得の具体的方法は、上記Ｍａｎｉａｔｉｓの実験書に従った。

【０１１９】

（２）マウスＡＴＤＣ５細胞からのＲＮＡ調製

マウスＥＣ（ｅｍｂｒｙｏｎａｌ　ｃａｒｃｉｎｏｍａ）由来クローン化細胞株ＡＴＤＣ５（Ａｔｓｕｍｉ,Ｔ.ｅｔ ａｌ.：Ｃｅｌｌ Ｄｉｆｆ.Ｄｅｖ.,30:ｐ109-116(1990)）を１０ｃｍシャーレ５０枚まで継代培養した後、上記（１）と同様の方法でポリＡ＋ＲＮＡを取得した。

【０１２０】

（３）オリゴキャッピング法による完全長ｃＤＮＡライブラリー作製

上記ヒト肺線維芽細胞とＡＴＤＣ５細胞のポリＡ＋ＲＮＡから、オリゴキャッピング法により完全長ｃＤＮＡライブラリーをそれぞれ作製した。オリゴキャッピング法による完全長ｃＤＮＡライブラリー作製の具体的方法は、菅野らの方法〔たとえば、Ｍａｒｕｙａｍａ, Ｋ. ＆ Ｓｕｇａｎｏ, Ｓ. Ｇｅｎｅ, １３８：１７１－１７４（１９９４）、Ｓｕｚｕｋｉ、Ｙ. ｅｔ ａｌ. Ｇｅｎｅ、２

００：１４９－１５６（１９９７）、鈴木・菅野　実験医学別冊　遺伝子工学ハンドブック改訂第３版］に従って作製した。

【０１２１】

（４）プラスミドＤＮＡの調製

　上記実施例で作製した完全長ｃＤＮＡライブラリーを、エレクトロポレーション法によって大腸菌ＴＯＰ１０株に形質転換した後、１００μｇ／ｍｌアンピシリンを含有するＬＢ寒天培地に塗布し、３７℃で一晩インキュベートした。続いて、アンピシリン含有ＬＢ寒天培地上で生育した大腸菌のコロニーから、ＱＩＡ ＧＥＮ社のＱＩＡｗｅｌｌ　９６　Ｕｌｔｒａ　Ｐｌａｓｍｉｄ　Ｋｉｔを用いてプラスミドを回収した。具体的方法は、ＱＩＡｗｅｌｌ　９６　Ｕｌｔｒａ　Ｐｌａｓｍｉｄ　Ｋｉｔに添付のプロトコールに従った。

【０１２２】

（実施例２）ＮＦ－κＢを活性化する作用を有するＤＮＡのクローニング

（１）ＮＦ－κＢを活性化する作用を有するタンパク質をコードするｃＤＮＡのスクリーニング

　２９３－ＥＢＮＡ細胞（Ｉｎｖｉｔｒｏｇｅｎ社より購入）を細胞培養用９６穴プレートに１×10^4Ｃｅｌｌｓ／ｗｅｌｌとなるように、５％ＦＢＳ存在下のＤＭＥＭ培地を用い、２４時間３７℃で培養した（５％CO_2存在下）。次いで、ＦｕＧＥＮＥ６（Ｒｏｃｈｅ社より購入）を用いて、ｐＮＦκＢ－Ｌｕｃ（ＳＴＲＡＴＡＧＥＮＥ社より購入）５０ｎｇと、上記実施例１．（４）で調製した完全長ｃＤＮＡ２μｌを１ウエルに共導入した。導入の方法は添付のプロトコールに従った。２４時間３７℃で培養後、ロングタームルシフェラーゼアッセイシステム、ピッカジーンＬＴ２．０（東洋インキ社）を用いて添付されている説明書に従い、ＮＦ－κＢのレポーター活性（ルシフェラーゼ活性）を測定した。なおルシフェラーゼ活性は、Ｐｅｒｋｉｎ　Ｅｌｍｅｒ社のＷａｌｌａｃ　ＡＲ ＶＯＴＭＳＴ　１４２０　ＭＵＬＴＩＬＡＢＥＬ　ＣＯＵＮＴＥＲを用いて行った。

【０１２３】

（２）ヌクレオチド配列の決定

　上記スクリーニングを１５５０００クローン行い、ルシフェラーゼ活性が対照実験（完全長ｃＤＮＡの代わりに、空ベクターｐＭＥ１８Ｓ－ＦＬ３を導入した細胞のルシフェラーゼ活性）と比べて５倍以上上昇しているプラスミドを選抜し、まず、クローニングされているｃＤＮＡの５’側（シークエンスプライマー：５’－ＣＴＴＣＴＧＣＴＣＴＡＡＡＡＧＣＴＧＣＧ－３’（配列番号１７９）と３’側（シークエンスプライマー：５’－ＣＧＡＣＣＴＧＣＡＧＣＴＣＧＡＧＣＡＣＡ－３’（配列番号１８０））からそれぞれｏｎｅ－ｐａｓｓシークエンスを行ない、できる限り長く決定した。なお、ヌクレオチド配列決定のための試薬や方法は、Ｔｈｅｒｍｏ　Ｓｅｑｕｅｎａｓｅ　ＩＩ　Ｄｙｅ　Ｔｅｒｍｉｎａｔｏｒ　Ｃｙｃｌｅ　Ｓｅｑｕｅｎｃｉｎｇ　Ｋｉｔ（アマシャム　ファルマシア社）、あるいはＢｉｇＤｙｅ　Ｔｅｒｍｉｎａｔｏｒ　Ｃｙｃｌｅ　Ｓｅｑｕｅｎｃｉｎｇ　ＦＳ　Ｒｅａｄｙ　Ｒｅａｃｔｉｏｎ　Ｋｉｔ（アプライドバイオシステムズ社）を用い、ＡＢＩ　ＰＲＩＳＭ　３７７シークエンサー、あるいは、ＡＢＩ　ＰＲＩＳＭ　３１００シークエンサーを用い、各々キットに添付されている説明書に従って行なった。

　　　【０１２４】

（３）得られたクローンのデータベース解析

　得られたヌクレオチド配列について、ＧｅｎＢａｎｋに対するＢＬＡＳＴ（Basic local alignment search tool）〔S. F. Altschul et al., J. Mol. Biol., 215: 403-410 (1990)〕検索を行なった。その結果、１４７クローンがＮＦ－κＢを活性化する作用を有する新規のタンパク質をコードする８９種類の遺伝子であった。

　　　【０１２５】

（４）全長シークエンス

　８９種類の新規のクローンについて全長ヌクレオチド配列（配列番号２、４、６、８、１０、１２、１４、１６、１８、２０、２２，２４、２６、２８、３０、３２、３４、３６、３８、４０、４２、４４、４６、４８、５０、５２、５４、５６、５８、６０、６２、６４、６６、６８、７０、７２、７４、７６、７８、８０、８２、８４、８６、８８、９０、９２、９４、９６、９８、１００、１

０２、１０４、１０６、１０８、１１０、１１２，１１４、１１６、１１８、１

２０、１２２、１２４、１２６、１２８、１３０、１３２、１３４、１３６、１

３８、１４０、１４２、１４４、１４６、１４８、１５０、１５１、１５３、１

５５、１５７、１５９、１６１、１６３、１６５、１６７、１６９、１７１、１

７３、１７５または１７７）を決定し、タンパク質をコードする部分（オープン

リーディングフレーム）のアミノ酸配列（配列番号１、３、５、７、９、１１、

１３、１５、１７、１９、２１、２３、２５、２７、２９、３１、３３、３５、

３７、３９、４１、４３、４５、４７、４９、５１、５３、５５、５７、５９、

６１、６３、６５、６７、６９、７１、７３、７５、７７、７９、８１、８３、

８５、８７、８９、９１、９３、９５、９７、９９、１０１、１０３、１０５、

１０７、１０９、１１１、１１３、１１５、１１７、１１９、１２１、１２３、

１２５、１２７、１２９、１３１、１３３、１３５、１３７、１３９、１４１、

１４３、１４５、１４７、１４９、１５２、１５４、１５６、１５８、１６０、

１６２、１６４、１６６、１６８、１７０、１７２、１７４、１７６および１７

８）を予想した。

【０１２６】

（実施例３）ＮＦ－κＢの活性化を阻害する化合物のスクリーニング

２９３－ＥＢＮＡ細胞を細胞培養用９６ｗｅｌｌプレートに、1×10^4Ｃｅ

ｌｌｓ／１００μｌ／ｗｅｌｌの細胞数になるように、５％ＦＢＳ存在下のＤＭ

ＥＭ培地にまき、５％CO_2存在下、３７℃で２４時間培養した。次いで、Ｆｕ

ＧＥＮＥ６を用いて、上記実施例２で得た、配列番号４１のＮＦ－κＢを活性化

する作用を有するタンパク質をコードする遺伝子を含有するプラスミド１０ｎｇ

と、レポータープラスミドｐＮＦκＢ－Ｌｕｃ５０ｎｇを１ｗｅｌｌに共導入し

た。１時間後、プロテアソーム阻害剤であることが知られているＭＧ１３２（Ｃ

ＡＬＢＩＯＣＨＥＭより購入）（Ｕｅｈａｒａ　Ｔ．ｅｔ．ａｌ．Ｊ．Ｂｉｏｌ

．Ｃｈｅｍ．　２７４　ｐ１５８７５－１５８８２（１９９９）、Ｗａｎｇ　Ｘ

Ｃ．ｅｔ　ａｌ．Ｉｎｖｅｓｔ．Ｏｐｈｔｈａｌｍｏｌ．Ｖｉｓ．Ｓｃｉ．４０

　ｐ４７７－４８６）を終濃度１０μＭになるように培養液中に加えた。３７℃

で２４時間培養後、ピッカジーンＬＴ２．０を用いてレポーター活性を測定した

。その結果、ＭＧ１３２はレポーター遺伝子の発現を抑制した（図１）。

【０１２７】

【発明の効果】

　本発明により、産業上有用性の高いＮＦ－κＢを活性化する作用を有するタンパク質やそれらの遺伝子が提供された。本発明のタンパク質やそれらの遺伝子により、ＮＦ－κＢの過剰な活性化、又は阻害が関与する疾患の治療や予防に有用な化合物のスクリーニング、さらにそのような疾患の診断薬を作製することが可能である。更に本発明の遺伝子は、遺伝子治療に用いられる遺伝子ソースとしても有用である。

【１２８】

【配列表】

SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA

<120> Novel Gene

<130> X13-994

<160> 180

<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser
            35   40   45

Ala Gly Pro Pro Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln
        50   55   60

Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly
65   70   75   80

Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly
                85   90   95

Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr
                100   105   110

Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
            115   120   125

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser
            130   135   140

Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly
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ggattcctgt aac atg agt gga ttg att acc atc gtg gta ctc ctt ggg   229
             Met Ser Gly Leu Ile Thr Ile Val Val Leu Leu Gly
             1   5   10

atc gcc ttt gta gtc tat aag ctg ttc ctg agt gac ggg cag tat tct   277
Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser Asp Gly Gln Tyr Ser
        15   20   25

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cct cca ccg tac tct gag tat cct cca ttt tcc cac cgt tac cag aga     325
Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe Ser His Arg Tyr Gln Arg
    30              35                  40


ttc acc aac tca gca gga cct cct ccc cca ggc ttt aag tct gag ttc     373
Phe Thr Asn Ser Ala Gly Pro Pro Pro Gly Phe Lys Ser Glu Phe
    45              50                  55                  60


aca gga cca cag aat act ggc cat ggt gca act tct ggt ttt ggc agt     421
Thr Gly Pro Gln Asn Thr Gly His Gly Ala Thr Ser Gly Phe Gly Ser
                65                  70                  75


gct ttt aca gga caa caa gga tat gaa aat tca gga cca ggg ttc tgg     469
Ala Phe Thr Gly Gln Gln Gly Tyr Glu Asn Ser Gly Pro Gly Phe Trp
                80                  85                  90


aca ggc ttg gga act ggt gga ata cta gga tat ttg ttt ggc agc aat     517
Thr Gly Leu Gly Thr Gly Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn
                95                 100                 105


aga gcg gca aca ccc ttc tca gac tcg tgg tac tac ccg tcc tat cct     565
Arg Ala Ala Thr Pro Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro
           110                 115                 120


ccc tcc tac cct ggc acg tgg aat agg gct tac tca ccc ctt cat gga     613
Pro Ser Tyr Pro Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly
125                 130                 135                 140


ggc tcg ggc agc tat tcg gta tgt tca aac tca gac acg aaa acc aga     661
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Gly Ser Gly Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg
          145   150   155

act gca tca gga tat ggt ggt acc agg aga cga taaagtagaa agttggagtc 714
Thr Ala Ser Gly Tyr Gly Gly Thr Arg Arg Arg
          160   165

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<213> Homo sapiens

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                20   25   30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
                35   40   45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
        50   55   60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65   70   75   80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
                85   90   95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
          100   105   110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
          115   120   125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
          130   135   140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145   150   155   160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
              165   170   175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
          180   185   190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Tyr Ser Glu Tyr Pro
          195   200   205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
          210   215   220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225   230   235   240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
              245   250   255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
             260   265   270

Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
             275   280   285

Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
             290   295   300

Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
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Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
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                                                             Met
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gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly
            5   10   15

ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp
         20   25   30

cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr
       35   40   45

gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys
50   55   60   65

tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile
            70   75   80

cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys

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                    85                      90                      95

aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc    453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser
        100                     105                     110


tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct    501
Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser
        115                     120                     125


tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa    549
Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
130                     135                     140                     145


ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat    597
Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
                150                     155                     160


tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att    645
Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
                165                     170                     175


acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc    693
Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
        180                     185                     190


ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca    741
Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
        195                     200                     205
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ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc   789
Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
210   215   220   225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt   837
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
             230   235   240

gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa   885
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
             245   250   255

aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta   933
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu
             260   265   270

gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg   981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser
         275   280   285

tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg   1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg
290   295   300   305

gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca   1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser
             310   315   320

aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg　　1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg
　　　　　　325　　　　　　　　　　　330　　　　　　　　　　335

aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggattttt　　1181
Arg Arg

catcactttc tctttagaaa aaaagtacta cctgttaaca attgggaaaa ggggatattc 1241

aaaagttcgg tggtgttatg tccagtgtag ctttttgtat tctattattt gaggctaaaa 1301

gttgatgtgt gacaaaatac ttatgtgttg tatgtcagtg taacatgcag atgtatattg 1361

cagttttتga aagtgatcat tactgtggaa tgctaaaaat acattaattt ctaaaacctg 1421

tgatgcccta agaagcatta agaatgaagg tgttgtacta atagaaacta agtacagaaa 1481

atttcagttt taggtggttg tagctgatga gttattacct catagagact gtaatattct 1541

atttggtatt atattatttg atgtttgctg ttcttcaaac atttaaatca agctttggac 1601

taattatgct aatttgtgag ttctgatcac ttttgagctc tgaagctttg aatcattcag 1661

tggtggagat ggccttctgg taactgaata ttaccttctg taggaaaagg tggaaaataa 1721

gcatctagaa ggttgttgtg aatgactctg tgctggcaaa aatgcttgaa acctctatat 1781

ttctttcgtt cataagaggt aaaggtcaaa tttttcaaca aaagtctttt aataacaaaa 1841

gcatgcagtt ctctgtgaaa tctcaaatat tgttgtaata gtctgtttca atcttaaaaa 1901

gaatcaataa aaacaaacaa ggg   1924

<210> 5

<211> 127

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1   5   10   15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
                35   40   45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                85   90   95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
　　　　　　　100　　　　　　　　　105　　　　　　　　　110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
　　　　115　　　　　　　　120　　　　　　　　125

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<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(605)

<400> 6

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca 236
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　Met Ala Gly Ala
　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　　1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile

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        5                      10                     15                     20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
                    25                     30                     35


cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
                    40                     45                     50


gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
                    55                     60                     65


aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
                    70                     75                     80


att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
    85                     90                     95                    100


atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg   572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu
                   105                    110                    115


gac att gcc ttc aag cta aac aac caa atc agt taagtgtact ctcctctcat 625
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Ser
                   120                    125
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ccctttcttc cctttgagca ttgccctctt tgggttcttt ttgagccaat tctaataaaa 685

gtaaaaatgg taatagt   702

<210> 7

<211> 233

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1   5   10   15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
                35   40   45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
                85   90   95

Pro Leu Pro His Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe
         100   105   110

Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu
         115   120   125

Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala
         130   135   140

Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu
145   150   155   160

Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr
         165   170   175

Tyr Glu Cys Asp Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly
         180   185   190

Val Val Leu Glu Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser
         195   200   205

Gly Lys Ser His Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr
         210   215   220

Pro Ser Gly Met Val Phe His Arg Val
225   230

<210> 8

<211> 2409

<212> DNA

<213> Homo sapiens

<220>

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<222> (225)..(923)

<400> 8

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cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca 236
                                             Met Ala Gly Ala
                                              1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5   10   15   20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
               25   30   35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat 380

Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

          40   45   50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

          55   60   65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

          70   75   80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

          85   90   95   100

atg gag atg agt cct tgg ttc caa ttc atg ctg ttt atc ctg cag ctg   572
Met Glu Met Ser Pro Trp Phe Gln Phe Met Leu Phe Ile Leu Gln Leu

                      105   110   115

gac att gcc ttc aag cta aac aac caa atc aga gaa aat gca gaa gtc   620
Asp Ile Ala Phe Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val

                      120   125   130

tcc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg   668
Ser Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp

                      135   140   145

act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc   716
Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe

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         150                    155                    160


aca tct ccc aag act cca gag cat gag ggc cgt tac tat gaa tgt gat    764
Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp
165                    170                    175                    180


gtc ctt cct tac gcc cag cat ctt cat cat tat ggt gtg gta ttg gag    812
Val Leu Pro Tyr Ala Gln His Leu His His Tyr Gly Val Val Leu Glu
                      185                    190                    195


gag gat cac cat gat gtc ccg acc ccc agt gct tct gga aaa agt cat    860
Glu Asp His His Asp Val Pro Thr Pro Ser Ala Ser Gly Lys Ser His .
                      200                    205                    210


ctt tgc cct tgg gat ttc cat gac ctt tat caa tat ccc agt gga atg    908
Leu Cys Pro Trp Asp Phe His Asp Leu Tyr Gln Tyr Pro Ser Gly Met
                      215                    220                    225


gtt ttc cat cgg gtt tgactggacc tggatgctgc tgtttggtga catccgacag    963
Val Phe His Arg Val
    230


ggcatcttct atgcgatgct tctgtccttc tggatcatct tctgtggcga gcacatgatg   1023


gatcagcacg agcggaacca catcgcaggg tattggaagc aagtcggacc cattgccgtt   1083


ggctccttct gcctcttcat atttgacatg tgtgagagag gggtacaact cacgaatccc   1143


ttctacagta tctggactac agacattgga acagagctgg ccatggcctt catcatcgtg   1203
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gctggaatct gcctctgcct ctacttcctg tttctatgct tcatggtatt tcaggtgttt 1263

cggaacatca gtgggaagca gtccagcctg ccagctatga gcaaagtccg gcggctacac 1323

tatgaggggc taattttttag gttcaagttc ctcatgctta tcaccttggc ctgcgctgcc 1383

atgactgtca tcttcttcat cgttagtcag gtaacggaag gccattggaa atggggcggc 1443

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aatggcgatc tgggtgtcca tagtgggggaa gaactccagc tcaccaccac tatcacccat 1623

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accagcggca tggacatttg tcagtttgcc ttctgacggt agcttttgga ggaagattcc 1863

tgcagccact aatgcattgt gtatgataac aaaaactctg gtatgacaca ttttctgtga 1923

tcattgttaa ttagtgacat agtaacatct gtagcagctg gttagtaaac ctcatgtggg 1983

ggtgggggtgg gggtgtattc cttggggggat ggtttgggcc gaatggggag tggaatatttt 2043

gacattttttc ctgtttttaaa ttctaggata gatttttaaca tcctttgcgg tcccagtcca 2103

aggtaggctg gtgtcatagt cttctcactc ctaatccatg accactgttt ttttcctatt 2163

tatatcacca ggtagcccac tgagttaata tttaagttgt caatagataa gtgtccctgt 2223

tttgtggcat aatataactg aatttcatga gaagatttat tccaccaggg gtatttcagc 2283

tttgaaacca aatctgtgta tctaatacta accaatctgt tggatgtggg ttttaaaaaa 2343

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<210> 9

<211> 198

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu Ser
1   5   10   15

Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu Ser Asp
                20   25   30

Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile Cys Pro Pro
            35   40   45

Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn Ile Ser Gln Lys
    50   55   60

Asp Cys Asp Cys Leu His Val Val Glu Pro Met Pro Val Arg Gly Pro
    65   70   75   80

Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu Cys Lys Tyr Glu Glu Arg
                85   90   95

Ser Ser Val Thr Ile Lys Val Thr Ile Ile Ile Tyr Leu Ser Ile Leu
                100   105   110

Gly Leu Leu Leu Leu Tyr Met Val Tyr Leu Thr Leu Val Glu Pro Ile
                115   120   125

Leu Lys Arg Arg Leu Phe Gly His Ala Gln Leu Ile Gln Ser Asp Asp
    130   135   140

Asp Ile Gly Asp His Gln Pro Phe Ala Asn Ala His Asp Val Leu Ala
145   150   155   160

Arg Ser Arg Ser Arg Ala Asn Val Leu Asn Lys Val Glu Tyr Ala Gln
                165   170   175

Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Ser Val Phe Asp
                180   185   190

Arg His Val Val Leu Ser

195

<210> 10

<211> 1498

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (86)..(679)

<400> 10

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ctgtgggacc gctgggcccc cagcg atg gcg acc ctg tgg gga ggc ctt ctt 112
　　　　　　　　　　　　　　　Met Ala Thr Leu Trp Gly Gly Leu Leu
　　　　　　　　　　　　　　　1　　　　　　　　　5

cgg ctt ggc tcc ttg ctc agc ctg tcg tgc ctg gcg ctt tcc gtg ctg 160
Arg Leu Gly Ser Leu Leu Ser Leu Ser Cys Leu Ala Leu Ser Val Leu
10　　　　　　　　15　　　　　　　　20　　　　　　　　25

ctg ctg gcg cag ctg tca gac gcc gcc aag aat ttc gag gat gtc aga 208
Leu Leu Ala Gln Leu Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg
　　　　　　　30　　　　　　　　35　　　　　　　　40

tgt aaa tgt atc tgc cct ccc tat aaa gaa aat tct ggg cat att tat 256
Cys Lys Cys Ile Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr

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                 45                      50                      55


aat aag aac ata tct cag aaa gat tgt gat tgc ctt cat gtt gtg gag   304
Asn Lys Asn Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu
            60                  65                  70


ccc atg cct gtg cgg ggg cct gat gta gaa gca tac tgt cta cgc tgt   352
Pro Met Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys
        75                  80                  85


gaa tgc aaa tat gaa gaa aga agc tct gtc aca atc aag gtt acc att   400
Glu Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
90                  95                  100                 105


ata att tat ctc tcc att ttg ggc ctt cta ctt ctg tac atg gta tat   448
Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val Tyr
                110                 115                 120


ctt act ctg gtt gag ccc ata ctg aag agg cgc ctc ttt gga cat gca   496
Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly His Ala
            125                 130                 135


cag ttg ata cag agt gat gat gat att ggg gat cac cag cct ttt gca   544
Gln Leu Ile Gln Ser Asp Asp Asp Ile Gly Asp His Gln Pro Phe Ala
            140                 145                 150


aat gca cac gat gtg cta gcc cgc tcc cgc agt cga gcc aac gtg ctg   592
Asn Ala His Asp Val Leu Ala Arg Ser Arg Ser Arg Ala Asn Val Leu
            155                 160                 165
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aac aag gta gaa tat gca cag cag cgc tgg aag ctt caa gtc caa gag    640
Asn Lys Val Glu Tyr Ala Gln Gln Arg Trp Lys Leu Gln Val Gln Glu
170             175             180             185


cag cga aag tct gtc ttt gac cgg cat gtt gtc ctc agc taattgggaa     689
Gln Arg Lys Ser Val Phe Asp Arg His Val Val Leu Ser
                190             195


ttgaattcaa ggtgactaga aagaaacagg cagacaactg gaaagaactg actgggtttt 749

gctgggtttc attttaatac cttgttgatt tcaccaactg ttgctggaag attcaaaact 809

ggaagcaaaa acttgcttga tttttttttc ttgttaacgt aataatagag acatttttaa 869

aagcacacag ctcaaagtca gccaataagt cttttcctat ttgtgacttt tactaataaa 929

aataaatctg cctgtaaatt atcttgaagt cctttacctg gaacaagcac tctctttttc 989

accacatagt tttaacttga ctttcaagat aattttcagg gtttttgttg ttgttgtttt 1049

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tcaagtcact ttactaaaca aacttttgta aatagacctt accttctatt ttcgagtttc 1169

atttatattt tgcagtgtag ccagcctcat caaagagctg acttactcat ttgacttttg 1229

cactgactgt attatctggg tatctgctgt gtctgcactt catggtaaac gggatctaaa 1289
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atgcctggtg gctttcaca aaaagcagat tttcttcatg tactgtgatg tctgatgcaa 1349

tgcatcctag aacaaactgg ccatttgcta gtttactcta aagactaaac atagtcttgg 1409

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<210> 11

<211> 221

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Leu Ala Ala Leu Ala Ala Val Glu Pro Ala Cys Gly
1   5   10   15

Ser Arg Tyr Gln Gln Leu Gln Asn Glu Glu Glu Ser Gly Glu Pro Glu
                20   25   30

Gln Ala Ala Gly Asp Ala Pro Pro Pro Tyr Ser Ser Ile Ser Ala Glu
            35   40   45

Ser Ala Ala Tyr Phe Asp Tyr Lys Asp Glu Ser Gly Phe Pro Lys Pro
        50   55   60

Pro Ser Tyr Asn Val Ala Thr Thr Leu Pro Ser Tyr Asp Glu Ala Glu
65   70   75   80

Arg Thr Lys Ala Glu Ala Thr Ile Pro Leu Val Pro Gly Arg Asp Glu
                85   90   95

Asp Phe Val Gly Arg Asp Asp Phe Asp Asp Ala Asp Gln Leu Arg Ile
               100   105   110

Gly Asn Asp Gly Ile Phe Met Leu Thr Phe Phe Met Ala Phe Leu Phe
               115   120   125

Asn Trp Ile Gly Phe Phe Leu Ser Phe Cys Leu Thr Thr Ser Ala Ala
               130   135   140

Gly Arg Tyr Gly Ala Ile Ser Gly Phe Gly Leu Ser Leu Ile Lys Trp
145   150   155   160

Ile Leu Ile Val Arg Phe Ser Thr Tyr Phe Pro Gly Tyr Phe Asp Gly
               165   170   175

Gln Tyr Trp Leu Trp Trp Val Phe Leu Val Leu Gly Phe Leu Leu Phe
               180   185   190

Leu Arg Gly Phe Ile Asn Tyr Ala Lys Val Arg Lys Met Pro Glu Thr
               195   200   205

Phe Ser Asn Leu Pro Arg Thr Arg Val Leu Phe Ile Tyr
               210   215   220

<210> 12

<211> 1864

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(815)

<400> 12

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gctcgctctg cttccctgct gccggctgcg cc atg gcg ttg gcg ttg gcg gcg   173
                                    Met Ala Leu Ala Leu Ala Ala
                                     1   5

ctg gcg gcg gtc gag ccg gcc tgc ggc agc cgg tac cag cag ttg cag   221
Leu Ala Ala Val Glu Pro Ala Cys Gly Ser Arg Tyr Gln Gln Leu Gln
             10   15   20

aat gaa gaa gag tct gga gaa cct gaa cag gct gca ggt gat gct cct   269
Asn Glu Glu Glu Ser Gly Glu Pro Glu Gln Ala Ala Gly Asp Ala Pro
         25   30   35

cca cct tac agc agc att tct gca gag agc gca gca tat ttt gac tac   317
Pro Pro Tyr Ser Ser Ile Ser Ala Glu Ser Ala Ala Tyr Phe Asp Tyr
40   45   50   55

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aag gat gag tct ggg ttt cca aag ccc cca tct tac aat gta gct aca    365
Lys Asp Glu Ser Gly Phe Pro Lys Pro Pro Ser Tyr Asn Val Ala Thr
            60                  65                  70


aca ctg ccc agt tat gat gaa gcg gag agg acc aag gct gaa gct act    413
Thr Leu Pro Ser Tyr Asp Glu Ala Glu Arg Thr Lys Ala Glu Ala Thr
            75                  80                  85


atc cct ttg gtt cct ggg aga gat gag gat ttt gtg ggt cgg gat gat    461
Ile Pro Leu Val Pro Gly Arg Asp Glu Asp Phe Val Gly Arg Asp Asp
            90                  95                  100


ttt gat gat gct gac cag ctg agg ata gga aat gat ggg att ttc atg    509
Phe Asp Asp Ala Asp Gln Leu Arg Ile Gly Asn Asp Gly Ile Phe Met
            105                 110                 115


tta act ttt ttc atg gca ttc ctc ttt aac tgg att ggg ttt ttc ctg    557
Leu Thr Phe Phe Met Ala Phe Leu Phe Asn Trp Ile Gly Phe Phe Leu
120                 125                 130                 135


tct ttt tgc ctg acc act tca gct gca gga agg tat ggg gcc att tca    605
Ser Phe Cys Leu Thr Thr Ser Ala Ala Gly Arg Tyr Gly Ala Ile Ser
            140                 145                 150


gga ttt ggt ctc tct cta att aaa tgg atc ctg att gtc agg ttt tcc    653
Gly Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser
            155                 160                 165
```

acc tat ttc cct gga tat ttt gat ggt cag tac tgg ctc tgg tgg gtg 701
Thr Tyr Phe Pro Gly Tyr Phe Asp Gly Gln Tyr Trp Leu Trp Trp Val
      170   175   180

ttc ctt gtt tta ggc ttt ctc ctg ttt ctc aga gga ttt atc aat tat 749
Phe Leu Val Leu Gly Phe Leu Leu Phe Leu Arg Gly Phe Ile Asn Tyr
      185   190   195

gca aaa gtt cgg aag atg cca gaa act ttc tca aat ctc ccc agg acc 797
Ala Lys Val Arg Lys Met Pro Glu Thr Phe Ser Asn Leu Pro Arg Thr
200   205   210   215

aga gtt ctc ttt att tat taaagatgtt ttctggcaaa ggccttcctg 845
Arg Val Leu Phe Ile Tyr
      220

catttatgaa ttctctctca agaagcaaga gaacacctgc aggaagtgaa tcaagatgca 905

gaacacagag gaataatcac ctgctttaaa aaaataaagt actgttgaaa agatcatttc 965

tctctatttg ttcctaggtg taaaatttta atagttaatg cagaattctg taatcattga 1025

atcattagtg gttaatgttt gaaaaagctc ttgcaatcaa gtctgtgatg tattaataat 1085

gccttatata ttgtttgtag tcattttaag tagcatgagc catgtccctg tagtcggtag 1145

ggggcagtct tgctttattc atcctccatc tcaaaatgaa cttggaatta aatattgtaa 1205

gatatgtata atgctggcca ttttaaaggg gttttctcaa aagttaaact tttgctatga 1265

ctgtgttttt gcacataatc catatttgct gttcaagtta atctagaaat ttattcaatt 1325

ctgtatgaac acctggaagc aaaatcatag tgcaaaaata catttaaggt gtggtcaaaa 1385

ataagtcttt aattggtaaa taataagcat taatttttta tagcctgtat tcacaattct 1445

gcggtacctt attgtaccta agggattcta aaggtgttgt cactgtataa aacagaaagc 1505

actaggatac aaatgaagct taattactaa aatgtaattc ttgacactct ttctataatt 1565

agcgttcttc acccccaccc ccaccccac cccccttatt ttccttttgt ctcctggtga 1625

ttaggccaaa gtctgggagt aaggagagga ttaggtactt aggagcaaag aaagaagtag 1685

cttggaactt ttgagatgat ccctaacata ctgtactact tgcttttaca atgtgttagc 1745

agaaaccagt gggttataat gtagaatgat gtgctttctg cccaagtggt aattcatctt 1805

ggtttgctat gttaaaactg taaatacaac agaacattaa taaatatctc ttgtgtagc 1864

<210> 13

<211> 242

<212> PRT

<213> Homo sapiens

<400> 13

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn

```
    1                5                       10                      15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
            20                      25                      30

Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu
            35                      40                      45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
            50                      55                      60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
 65                      70                      75                      80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
                85                      90                      95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
            100                     105                     110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala
            115                     120                     125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
            130                     135                     140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145                     150                     155                     160
```

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
                165   170   175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
            180   185   190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
            195   200   205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
    210   215   220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225   230   235   240

Leu Leu

<210> 14

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 14

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gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg    51
              Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
               1           5                   10


ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca    99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
    15              20                  25


cct act tca aac cca gca ccg cag att gtg cag gct gcg tct tca gca    147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala
30              35                  40                  45


cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act    195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
                50                  55                  60


gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat    243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
                65                  70                  75


ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat    291
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
                80                  85                  90


gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa    339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
    95                  100                 105


aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc    387
```

```
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110             115             120             125
```

```
agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg   435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
                130             135             140
```

```
gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc   483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
                145             150             155
```

```
ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga   531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
                160             165             170
```

```
ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat   579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
        175             180             185
```

```
tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt   627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
190             195             200             205
```

```
ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta   675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
                210             215             220
```

```
aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg   723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
```

```
            225                    230                    235


tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat   778
Tyr Phe Phe Leu Leu
            240


gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact aataacagaa   838


gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta   898


caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata   958


tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag   1018


tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag   1078


tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa   1138


ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac   1198


atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg   1258


atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa   1318


taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc   1378


actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca   1438


cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa   1498
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```
ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttatttttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcattgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtgggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacatttttc 2218

catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

cattgtcttt gataaataaa acagttttgt tttgctaata tagcct        2324
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<210> 15

<211> 242

<212> PRT

<213> Homo sapiens

<400> 15

Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn
1   5   10   15

Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser
                20   25   30

Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu
            35   40   45

Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val
        50   55   60

Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro
65   70   75   80

Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu
                85   90   95

Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln
                100   105   110

Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala

```
            115                    120                    125

Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe
    130                    135                    140

Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile
145                    150                    155                    160

Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu
                   165                    170                    175

Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr
                180                    185                    190

Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu
                195                    200                    205

Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg
    210                    215                    220

Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe
225                    230                    235                    240

Leu Leu
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<210> 16

<211> 2324

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (13)..(738)

<400> 16

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gagccgggca gg atg gat cac cac cag ccg ggg act ggg cgc tac cag gtg    51
           Met Asp His His Gln Pro Gly Thr Gly Arg Tyr Gln Val
            1               5                   10


ctt ctt aat gaa gag gat aac tca gaa tca tcg gct ata gag cag cca    99
Leu Leu Asn Glu Glu Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro
     15                  20                  25


cct act tca aac cca gca ccg cag att gtg cag gct gtg tct tca gca    147
Pro Thr Ser Asn Pro Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala
 30                  35                  40                  45


cca gca ctt gaa act gac tct tcc cct cca cca tat agt agt att act    195
Pro Ala Leu Glu Thr Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr
                 50                  55                  60


gtg gaa gta cct aca act tca gat aca gaa gtt tac ggt gag ttt tat    243
Val Glu Val Pro Thr Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr
                 65                  70                  75


ccc gtg cca cct ccc tat agc gtt gct acc tct ctt cct aca tac gat    291
```

```
Pro Val Pro Pro Pro Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp
         80                  85                  90


gaa gct gag aag gct aaa gct gct gca atg gca gct gca gca gca gaa   339
Glu Ala Glu Lys Ala Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu
         95                 100                 105


aca tct caa aga att cag gag gaa gag tgt cca cca aga gat gac ttc   387
Thr Ser Gln Arg Ile Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe
110                 115                 120                 125


agt gat gca gac cag ctc aga gtg ggg aat gat ggc att ttc atg ctg   435
Ser Asp Ala Asp Gln Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu
                130                 135                 140


gca ttt ttc atg gca ttt att ttc aac tgg ctt gga ttt tgt tta tcc   483
Ala Phe Phe Met Ala Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser
                145                 150                 155


ttc tgt atc acc aat acc ata gct gga agg tat ggt gct atc tgc gga   531
Phe Cys Ile Thr Asn Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly
                160                 165                 170


ttt ggc ctt tcc ttg atc aaa tgg atc ctt att gtc agg ttt tct gat   579
Phe Gly Leu Ser Leu Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp
                175                 180                 185


tat ttt act gga tat ttc aat gga cag tat tgg ctt tgg tgg ata ttt   627
Tyr Phe Thr Gly Tyr Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe
```

190   195   200   205

ctt gta ctt ggc ctg ctc ctt ttc ttc aga gga ttt gtt aat tat cta   675
Leu Val Leu Gly Leu Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu
                    210   215   220

aaa gtc aga aac atg tct gaa agt atg gca gct gct cat aga aca agg   723
Lys Val Arg Asn Met Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg
                    225   230   235

tat ttc ttc tta ttg tagagactgc atcaacccga cattcctttc ttataccaat   778
Tyr Phe Phe Leu Leu
        240

gtgaaatttc cagatcatct gtaaacctac aactttaata gaagactact ataacagaa   838

gacaaattag tgaagaaaag acggagtttc gaaattgaat ggcagggtgg tttttgctta   898

caagccattt ctgttcattc tttaagtatc tatatttcat ttgttttgca catatgcata   958

tgtgcccatt taagatattt gcatatactt gatagaaacc ataaagttgt agcagttaag   1018

tccagtcaca tttggttaat cagtgtttga tataattgaa agagttgagt ggataaacag   1078

tcttccagct tgtaaatgcc attgacttct gacctgacat ttagtataat aaaaatgaaa   1138

ttcttaacca tgtcaaatga tttagtttct ggctcttaga ctcatctggc agttctacac   1198

atgaaacatc ttttgttata tagggtgtat tgaaacctgc agtgctgatt attagaaagg   1258

atttgtcaga tttttgaaca tgatatttac attattattt aggaaaactc ttcctgtaaa 1318

taaccatgca taacttactt tctgcaatgt tttcttagaa attgtgtcca gatagctttc 1378

actaatttta aattaagtga actaaatata tatgtgtata tgtatacaca tatatataca 1438

cacacacata tatatattta gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa 1498

ttttaagaaa atgtgggaat accaaatgtc ctttataaga aaaataaatt ttattttaag 1558

ggacatacta gttttaggga ttttcagatg ggaagctgca tttttaggat tgcccatctt 1618

aagagatctt gcaggaagag attgtattag atattatatt tatttcattt aagataattt 1678

tcaaagttaa ttttctaaat aagataattc tcattgtgt ttgtctttta aaaggccaat 1738

aaaatatctt tcagtatcat tgtaataatt ttttagagtt taatttgtaa agcttagcaa 1798

ataaaatctt gtactatgaa tagcttcttg ctttatgact ttaggattaa cttgtaaaaa 1858

acatatcctg aactgagata tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg 1918

gcatatagga ctgtggggtc tgtgtgtgta gtgagagtgt gtagccacta ttataactgg 1978

aatttaattt acattcataa actactatat ttcccatctt gcaaatcatt ttatgtctca 2038

tctgtttttc ctttcggtta tatctttggt tttgaatacc aacatttaaa atgatggtat 2098

tttatctttt aaacttaaaa attatttaat acagctatat ggaccttata aaattgattt 2158

cttatttatt attagacatt actactaaaa ggtacatcta actattcagg gacattttc 2218

catttccaaa aaataaaatt tattatgctt tataacctct tctgtatttt ctaatttttt 2278

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<210> 17

<211> 336

<212> PRT

<213> Homo sapiens

<400> 17

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met
1   5   10   15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr
            20   25   30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu
        35   40   45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro
    50   55   60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly
65   70   75   80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp
                85   90   95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu
                100   105   110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro
                115   120   125

Ala Pro Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr
        130   135   140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145   150   155   160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
                165   170   175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
                180   185   190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
                195   200   205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
                210   215   220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala

```
        225                    230                    235                    240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
                    245                    250                    255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
                    260                    265                    270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr
                    275                    280                    285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
         290                    295                    300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305                    310                    315                    320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
                    325                    330                    335
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<210> 18

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 18

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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat   106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
         5   10   15

agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg   154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
        20   25   30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg   202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
   35   40   45   50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg   250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                55   60   65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
                70   75   80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
                85   90   95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
    100   105   110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115   120   125   130

cag att gtg cag gct gtg tct tca gca cca gca ctt gaa act gac tct   490
Gln Ile Val Gln Ala Val Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
         135   140   145

tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca   538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
         150   155   160

gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc   586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
         165   170   175

gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct   634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
    180   185   190

gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag   682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195   200   205   210

gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga　　730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
　　　　　　　　215　　　　　　　　　220　　　　　　　　　225

gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att　　778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
　　　　　　　　230　　　　　　　　　235　　　　　　　　　240

ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata　　826
Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
　　　　　　　　245　　　　　　　　　250　　　　　　　　　255

gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa　　874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
　　　　　　　　260　　　　　　　　　265　　　　　　　　　270

tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat　　922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275　　　　　　　　　280　　　　　　　　　285　　　　　　　　　290

gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt　　970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
　　　　　　　　295　　　　　　　　　300　　　　　　　　　305

ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa　　1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
　　　　　　　　310　　　　　　　　　315　　　　　　　　　320

agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg　　1060

Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
       325   330   335

tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct 1120

gtaaacctac aactttaata gaagactact ataacagaa gacaaattag tgaagaaaag 1180

acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc 1240

tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt taagatattt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc 1420

attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga 1480

tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata 1540

taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca 1600

tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt 1660

tctgcaatgt tttcttagaa attgtgtcca gatagctttc actaatttta aattaagtga 1720

actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

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accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttagggga 1900

ttttcagatg ggaagctgca ttttaggat tgcccatctt aagagatctt gcaggaagag 1960

attgtattag atattatatt tatttcattt aagataattt tcaaagttaa ttttctaaat 2020

aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

tagcttcttg ctttatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200

tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgtttttc ctttcggtta 2380

tatctttggt tttgaatacc aacatttaaa atgatggtat tttatctttt aaacttaaaa 2440

attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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acagttttgt tttgct                                                  2636
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<210> 19

<211> 336

<212> PRT

<213> Homo sapiens

<400> 19

Met Ala Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met

1   5   10   15

Leu Asn Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr

                20   25   30

Asn Ala Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu

            35   40   45

Leu Pro Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro

        50   55   60

Ala Ala Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly

65   70   75   80

Glu Asp Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp

                85   90   95

His His Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu

                100   105   110

Asp Asn Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro

            115   120   125

Ala Pro Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr
130   135   140

Asp Ser Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr
145   150   155   160

Thr Ser Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro
                    165   170   175

Tyr Ser Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala
                180   185   190

Lys Ala Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile
                195   200   205

Gln Glu Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln
        210   215   220

Leu Arg Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala
225   230   235   240

Phe Ile Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn
                    245   250   255

Thr Ile Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu
                260   265   270

Ile Lys Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr

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         275                280                285

Phe Asn Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu
    290                295                300

Leu Leu Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met
305                310                315                320

Ser Glu Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
                   325                330                335
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<210> 20

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)..(1060)

<400> 20

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                                                          Met Ala
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cgc cgg cgg agc cag cga gtc tgc gcg agc ggt ccg agc atg ctc aat    106
Arg Arg Arg Ser Gln Arg Val Cys Ala Ser Gly Pro Ser Met Leu Asn
         5                10                15
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agc gcg cgc ggc gcc ccg gag ctt ctc cgc gga acc gcg acc aac gcg   154
Ser Ala Arg Gly Ala Pro Glu Leu Leu Arg Gly Thr Ala Thr Asn Ala
      20   25   30

gag gtc tcg gcg gcc gct gcg gga gcc aca gga agt gaa gag ctt ccg   202
Glu Val Ser Ala Ala Ala Ala Gly Ala Thr Gly Ser Glu Glu Leu Pro
  35   40   45   50

ccg gga gac cgc ggc tgc agg aac gga ggc gga agg ggc cct gcg gcg   250
Pro Gly Asp Arg Gly Cys Arg Asn Gly Gly Gly Arg Gly Pro Ala Ala
                  55   60   65

acg acg tcg tcg acg ggg gtg gcc gtg gga gct gag cac gga gaa gac   298
Thr Thr Ser Ser Thr Gly Val Ala Val Gly Ala Glu His Gly Glu Asp
              70   75   80

tcc ctc tct cgg aag ccg gat ccc gag ccg ggc agg atg gat cac cac   346
Ser Leu Ser Arg Lys Pro Asp Pro Glu Pro Gly Arg Met Asp His His
          85   90   95

cag ccg ggg act ggg cgc tac cag gtg ctt ctt aat gaa gag gat aac   394
Gln Pro Gly Thr Gly Arg Tyr Gln Val Leu Leu Asn Glu Glu Asp Asn
      100   105   110

tca gaa tca tcg gct ata gag cag cca cct act tca aac cca gca ccg   442
Ser Glu Ser Ser Ala Ile Glu Gln Pro Pro Thr Ser Asn Pro Ala Pro
115   120   125   130

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cag att gtg cag gct gcg tct tca gca cca gca ctt gaa act gac tct      490
Gln Ile Val Gln Ala Ala Ser Ser Ala Pro Ala Leu Glu Thr Asp Ser
                135                 140                 145


tcc cct cca cca tat agt agt att act gtg gaa gta cct aca act tca      538
Ser Pro Pro Pro Tyr Ser Ser Ile Thr Val Glu Val Pro Thr Thr Ser
                150                 155                 160


gat aca gaa gtt tac ggt gag ttt tat ccc gtg cca cct ccc tat agc      586
Asp Thr Glu Val Tyr Gly Glu Phe Tyr Pro Val Pro Pro Pro Tyr Ser
                165                 170                 175


gtt gct acc tct ctt cct aca tac gat gaa gct gag aag gct aaa gct      634
Val Ala Thr Ser Leu Pro Thr Tyr Asp Glu Ala Glu Lys Ala Lys Ala
        180                 185                 190


gct gca atg gca gct gca gca gca gaa aca tct caa aga att cag gag      682
Ala Ala Met Ala Ala Ala Ala Ala Glu Thr Ser Gln Arg Ile Gln Glu
195                 200                 205                 210


gaa gag tgt cca cca aga gat gac ttc agt gat gca gac cag ctc aga      730
Glu Glu Cys Pro Pro Arg Asp Asp Phe Ser Asp Ala Asp Gln Leu Arg
                215                 220                 225


gtg ggg aat gat ggc att ttc atg ctg gca ttt ttc atg gca ttt att      778
Val Gly Asn Asp Gly Ile Phe Met Leu Ala Phe Phe Met Ala Phe Ile
                230                 235                 240


ttc aac tgg ctt gga ttt tgt tta tcc ttc tgt atc acc aat acc ata      826
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Phe Asn Trp Leu Gly Phe Cys Leu Ser Phe Cys Ile Thr Asn Thr Ile
        245                 250                 255


gct gga agg tat ggt gct atc tgc gga ttt ggc ctt tcc ttg atc aaa    874
Ala Gly Arg Tyr Gly Ala Ile Cys Gly Phe Gly Leu Ser Leu Ile Lys
        260                 265                 270


tgg atc ctt att gtc agg ttt tct gat tat ttt act gga tat ttc aat    922
Trp Ile Leu Ile Val Arg Phe Ser Asp Tyr Phe Thr Gly Tyr Phe Asn
275                 280                 285                 290


gga cag tat tgg ctt tgg tgg ata ttt ctt gta ctt ggc ctg ctc ctt    970
Gly Gln Tyr Trp Leu Trp Trp Ile Phe Leu Val Leu Gly Leu Leu Leu
                295                 300                 305


ttc ttc aga gga ttt gtt aat tat cta aaa gtc aga aac atg tct gaa   1018
Phe Phe Arg Gly Phe Val Asn Tyr Leu Lys Val Arg Asn Met Ser Glu
        310                 315                 320


agt atg gca gct gct cat aga aca agg tat ttc ttc tta ttg           1060
Ser Met Ala Ala Ala His Arg Thr Arg Tyr Phe Phe Leu Leu
        325                 330                 335


tagagactgc atcaacccga cattcctttc ttataccaat gtgaaatttc cagatcatct   1120


gtaaacctac aactttaata gaagactact ataacagaa gacaaattag tgaagaaaag   1180


acggagtttc gaaattgaat ggcagggtgg tttttgctta caagccattt ctgttcattc   1240
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tttaagtatc tatatttcat ttgttttgca catatgcata tgtgcccatt taagatattt 1300

gcatatactt gatagaaacc ataaagttgt agcagttaag tccagtcaca tttggttaat 1360

cagtgtttga tataattgaa agagttgagt ggataaacag tcttccagct tgtaaatgcc 1420

attgacttct gacctgacat ttagtataat aaaaatgaaa ttcttaacca tgtcaaatga 1480

tttagtttct ggctcttaga ctcatctggc agttctacac atgaaacatc ttttgttata 1540

taaggtgtat tgaaacctgc agtgctgatt attagaaagg atttgtcaga tttttgaaca 1600

tgatatttac attattattt aggaaaactc ttcctgtaaa taaccatgca taacttactt 1660

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actaaatata tatgtgtata tgtatacaca tatatataca cacacacata tatatattta 1780

gaaacgtgag tgttaaagat agaatttgtt ttaggacaaa ttttaagaaa atgtgggaat 1840

accaaatgtc ctttataaga aaaataaatt ttgttttaag ggacatacca gttttaggga 1900

ttttcagatg ggaagctgca tttttaggat tgcccatctt aagagatctt gcaggaagag 1960

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aagataattc tcatttgtgt ttgtctttta aaaggccaat aaaatatctt tcagtatcat 2080

tgtaataatt ttttagagtt taatttgtaa agcttagcaa ataaaatctt gtactatgaa 2140

tagcttcttg ctttatgact ttaggattaa cttgtaaaaa acatatcctg aactgagata 2200

tgcaaaatac tcattttcaa gttatggaaa tgtgtttgtg gcatatagga ctgtggggtc 2260

tgtgtgtgta gtgagagtgt gtagccacta ttataactgg aatttaattt acattcataa 2320

actactatat ttcccatctt gcaaatcatt ttatgtctca tctgtttttc ctttcggtta 2380

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attatttaat acagctatat ggaccttata aaattgattt cttatttatt attagacatt 2500

actactaaaa ggtacatcta actattcagg gacatttttc catttccaaa aaataaaatt 2560

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<210> 21

<211> 76

<212> PRT

<213> Homo sapiens

<400> 21

Met Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr
1   5   10   15

Lys Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val
                20   25   30

Ser Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn
                35   40   45

Lys Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr
                50   55   60

Lys Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
        65   70   75

<210> 22

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (176)..(403)

<400> 22

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gcagagtcct aggcggtgcg cggcctcctg cctcctccct cctcggcggt cgcggcccgc 120

cggcctccgc ggtgcctgcc ttcgctctca ggttgaggag ctcaagcttg ggaaa atg 178

                                                                Met

1

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gtg tgc att cct tgt atc gtc att cca gtt ctg ctc tgg atc tac aaa    226
Val Cys Ile Pro Cys Ile Val Ile Pro Val Leu Leu Trp Ile Tyr Lys
            5                   10                  15


aaa ttc ctg gag cca tat ata tac cct ctg gtt tcc ccc ttc gtt agt    274
Lys Phe Leu Glu Pro Tyr Ile Tyr Pro Leu Val Ser Pro Phe Val Ser
            20                  25                  30


cgt ata tgg cct aag aaa gca ata caa gaa tcc aat gat aca aac aaa    322
Arg Ile Trp Pro Lys Lys Ala Ile Gln Glu Ser Asn Asp Thr Asn Lys
        35                  40                  45


ggc aaa gta aac ttt aag ggt gca gac atg aat gga tta cca aca aaa    370
Gly Lys Val Asn Phe Lys Gly Ala Asp Met Asn Gly Leu Pro Thr Lys
    50                  55                  60                  65


gga cca aca gaa atc tgt gat aaa aag aaa gac taaagaaatt ttcctaaagg  423
Gly Pro Thr Glu Ile Cys Asp Lys Lys Lys Asp
                70                  75


accccatcat ttaaaaaatg gacctgataa tatgaagcat cttccttgta attgtctctg  483

accttttat ctgagaccgg aattcaggat aggagtctag atatttacct gatactaatc  543

aggaaatata tgatatccgt atttaaaatg tagttagtta tatttaatga cctcattcct  603

aagttccttt ttcgttaatg tagctttcat ttctgttatt gctgtttgaa taatatgatt  663
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aaatagaagg tttgtgccag tagacattat gttactaaat cagcacttta aaatctttgg 723

ttctctaatt catatgaatt tgctgtttgc tctaatttct ttgggctctt ctaatttgag 783

tggagtacaa ttttgttgtg aaacagtcca gtgaaactgt gcagggaaat gaaggtagaa 843

ttttgggagg taataatgat gtgaaacata aagatttaat aattactgtc caacacagtg 903

gagcagcttg tccacaaata tagtaattac tatttattgc tctaaggaag attaaaaaaa 963

gatagggaaa aggggggaaac ttctttgaaa aatgaaacat ctgttacatt aatgtctaat 1023

tataaaattt taatccttac tgcatttctt ctgttcctac aaatgtatta aacattcagt 1083

tt 1085

<210> 23

<211> 84

<212> PRT

<213> Homo sapiens

<400> 23

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1   5   10   15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
            20   25   30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile

       35   40   45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp

       50   55   60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His Ser

    65   70   75   80

Leu Ser Gly Leu

<210> 24

<211> 1593

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (65)..(316)

<400> 24

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cgcc atg gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc 109

     Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile

      1   5   10   15

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ctg ccg gaa att cag aag cca gag agg aag att cag ttt aag gag aaa   157
Leu Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys
            20              25              30


gtg ctg tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag   205
Val Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln
            35              40              45


att ccc ctg ttt ggg atc atg tct tca gat tca gct gac cct ttc tat   253
Ile Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr
            50              55              60


tgg atg aga gtg att cta gcc tct aac aga ggc aca ttg atg gag cac   301
Trp Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu His
            65              70              75


tct ctc tct ggc ctt tagggagtcc cctcttagga caggcactgc ccagcagcaa   356
Ser Leu Ser Gly Leu
    80


gggcagcaga gttgggtgct aagatcctga ggagctcgag gtttcgagct ggctttagac   416


attggtggga ccaaggatgt tttgcaggat gccctgatcc taagaagggg gcctgggggt   476


gcgtgcagcc tgtcggggag accccactct gtgcacctat tggctcttct agctgactct   536


tctcgttggg cttagagtct gcctgtttct gctagctccg tgtttagtcc acttgggtca   596
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出証特２００２−３０３２９３５

tcagctctgc caagctgagc ctggccaagc taggtggaca gacccttgca gtgatgtccg 656

tttgtccaga ttctgccagt catcactgga cacgtctcct cgcagctgcc ctagcaaggg 716

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aagggacaag aagggacttg cctaaagcca cccagcaact cagcagcaga accaagatgg 1136

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acccagtcct gagcagggga gaggctcttg agacctgatg ccctcctacc cacatggttc 1256

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<210> 25

<211> 179

<212> PRT

<213> Homo sapiens

<400> 25

Met Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu
1   5   10   15

Pro Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val
                20   25   30

Leu Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile
            35   40   45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala
        50   55   60

Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys
65   70   75   80

Thr Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln
                85   90   95

Leu Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met
         100   105   110

Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly
         115   120   125

Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile
         130   135   140

Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr
145   150   155   160

Phe Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala
                 165   170   175

Leu Leu Phe

<210> 26

<211> 1820

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (114)..(650)

<400> 26

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acgcggagca gagctgagct gaagcgggac ccggagcccg agcagccgcc gcc atg 116
                                                          Met
                                                          1

gca atc aaa ttt ctg gaa gtc atc aag ccc ttc tgt gtc atc ctg ccg 164
Ala Ile Lys Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro
            5   10   15

gaa att cag aag cca gag agg aag att cag ttt aag gag aaa gtg ctg 212
Glu Ile Gln Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu
        20   25   30

tgg acc gct atc acc ctc ttt atc ttc tta gtg tgc tgc cag att ccc 260
Trp Thr Ala Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro
        35   40   45

ctg ttt ggg atc atg tct tca gat tca gct gac ccg gtc cat gca gtt 308
Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Val His Ala Val
50   55   60   65

gta tac ata gtg ttc atg ctg ggc tcc tgt gca ttc ttc tcc aaa acg 356
Val Tyr Ile Val Phe Met Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr
                70   75   80

tgg att gag gtc tca ggt tcc tct gcc aaa gat gtt gca aag cag ctg 404
Trp Ile Glu Val Ser Gly Ser Ser Ala Lys Asp Val Ala Lys Gln Leu

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                85                    90                    95


aag gag cag cag atg gtg atg aga ggc cac cga gag acc tcc atg gtc    452
Lys Glu Gln Gln Met Val Met Arg Gly His Arg Glu Thr Ser Met Val
        100                   105                   110


cat gaa ctc aac cgg tac atc ccc aca gcc gcg gcc ttt ggt ggg ctg    500
His Glu Leu Asn Arg Tyr Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu
        115                   120                   125


tgc atc ggg gcc ctc tcg gtc ctg gct gac ttc cta ggc gcc att ggg    548
Cys Ile Gly Ala Leu Ser Val Leu Ala Asp Phe Leu Gly Ala Ile Gly
130                   135                   140                   145


tct gga acc ggg atc ctg ctc gca gtc aca atc atc tac cag tac ttt    596
Ser Gly Thr Gly Ile Leu Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe
                      150                   155                   160


gag atc ttc gtt aag gag caa agc gag gtt ggc agc atg ggg gcc ctg    644
Glu Ile Phe Val Lys Glu Gln Ser Glu Val Gly Ser Met Gly Ala Leu
                165                   170                   175


ctc ttc tgagcccgtc tcccggacag gttgaggaag ctgctccaga agcgcctcgg    700
Leu Phe


aaggggagct ctcatcatgg cgcgtgctgc tgcggcatat ggactttaa taatgttttt    760


gaatttcgta ttctttcatt ccactgtgta aagtgctaga cattttccaa tttaaaattt    820
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cagagaagtg ggaatggtat aggattgtcc ccaagtgtcc atgtaacttt tgttttaacc  940

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gggtgtgaag ctgggagcag atcatgtatt tcccggagac atgggacctt gctggcatgt 1120

ctccttcaca atcaggcgtg ggaatatctg gcttaggact gtttctctct aagacaccat 1180

tgttttccct tattttaaaa gtgatttttt taaggacaga acttcttcca aaagagaggg 1240

atggctttcc cagaagacac tctggagacc ttgctggcag tgctagccag gaaacagagt 1300

gaccaaggga caagaaggga cttgcctaaa gccacccagc aactcagcag cagaaccaag 1360

atgggcccca ggctcctcca tatggcccag ggcttaccac cctatcacac gtggccttgt 1420

ctagacccag tcctgagcag gggagaggct cttgagacct gatgccctcc tacccacatg 1480

gttctcccac tgccctgtct gctctgctgc tacaragggg cagggcctcc cccagcccac 1540

gcttaggaat gcttggcctc tggcaggcag gcagctgtac ccaagctggt gggcaggggg 1600

ctggaaggca ccaggcctca ggaggagccc catagtcccg cctgcagcct gtaaccatcg 1660

gctgggccct gcaaggccca cactcacgcc ctgtgggtga tggtcacggt gggtgggtgg 1720
```

gggctgaccc cagcttccag gggactgtca ctgtggacgc caaaatggca taactsasat 1780

aaggtgaata agtgacaaat aaagccagtt ttttacaagg   1820

<210> 27

<211> 279

<212> PRT

<213> Homo sapiens

<400> 27

```
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp
1               5                   10                  15


Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
            20                  25                  30


Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
        35                  40                  45


Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
    50                  55                  60


Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65                  70                  75                  80


Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
                85                  90                  95
```

Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
　　　　　　100　　　　　　　　　105　　　　　　　　　110

Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
　　　　　　115　　　　　　　　　120　　　　　　　　　125

Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
　　　　　　130　　　　　　　　　135　　　　　　　　　140

His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145　　　　　　　　　150　　　　　　　　　155　　　　　　　　　160

Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
　　　　　　　　165　　　　　　　　　170　　　　　　　　　175

Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
　　　　　　180　　　　　　　　　185　　　　　　　　　190

Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
　　　　　　195　　　　　　　　　200　　　　　　　　　205

Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
　　　　　　210　　　　　　　　　215　　　　　　　　　220

Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225　　　　　　　　　230　　　　　　　　　235　　　　　　　　　240

Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr

```
                245                  250                  255
```

Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
```
              260                  265                  270
```

Ile Ala Lys Val Lys Ala Asn
```
              275
```

<210> 28

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(955)

<400> 28

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tgctccctcc gagcgctccg ccgttgcccg cctggccccct acggagtcct tagccagg 118

```
atg gag gct gtt gtg aac ttg tac caa gag gtg atg aag cac gca gat    166
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp

  1               5                  10                  15
```

```
ccc cgg atc cag ggc tac cct ctg atg ggg tcc ccc ttg cta atg acc    214
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr
```

```
                    20                      25                       30

tcc att ctc ctg acc tac gtg tac ttc gtt ctc tca ctt ggg cct cgc   262
Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
            35                      40                      45


atc atg gct aat cgg aag ccc ttc cag ctc cgt ggc ttc atg att gtc   310
Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
            50                      55                      60


tac aac ttc tca ctg gtg gca ctc tcc ctc tac att gtc tat gag ttc   358
Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
65                      70                      75                      80


ctg atg tcg ggc tgg ctg agc acc tat acc tgg cgc tgt gac cct gtg   406
Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
                    85                      90                      95


gac tat tcc aac agc cct gag gca ctt agg atg gtt cgg gtg gcc tgg   454
Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
            100                     105                     110


ctc ttc ctc ttc tcc aag ttc att gag ctg atg gac aca gtg atc ttt   502
Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
            115                     120                     125


att ctc cga aag aaa gac ggg cag gtg acc ttc cta cat gtc ttc cat   550
Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
            130                     135                     140
```

出証特２００２－３０３２９３５

cac tct gtg ctt ccc tgg agc tgg tgg tgg ggg gta aag att gcc ccg   598
His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
145   150   155   160

gga gga atg ggc tct ttc cat gcc atg ata aac tct tcc gtg cat gtc   646
Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
           165   170   175

ata atg tac ctg tac tac gga tta tct gcc ttt ggc cct gtg gca caa   694
Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
           180   185   190

ccc tac ctt tgg tgg aaa aag cac atg aca gcc att cag ctg atc cag   742
Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
           195   200   205

ttt gtc ctg gtc tca ctg cac atc tcc cag tac tac ttt atg tcc agc   790
Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
         210   215   220

tgt aac tac cag tac cca gtc att att cac ctc atc tgg atg tat ggc   838
Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
225   230   235   240

acc atc ttc ttc atg ctg ttc tcc aac ttc tgg tat cac tct tat acc   886
Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
         245   250   255

```
aag ggc aag cgg ctg ccc cgt gca ctt cag caa aat gga gct cca ggt    934
Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
            260                 265                 270


att gcc aag gtc aag gcc aac tgagaagcat ggcctagata ggcgcccacc    985
Ile Ala Lys Val Lys Ala Asn
            275


taagtgcctc aggactgcac cttagggcag tgtccgtcag tgccctctcc acctacacct  1045

gtgaccaagg cttatgtggt caggactgag caggggactg gccctcccct ccccacagct  1105

gctctacagg gaccacggct ttggttcctc acccacttcc cccgggcagc tccagggatg  1165

tggcctcatt gctgtctgcc actccagagc tgggggctaa aagggctgta cagttatttc  1225

cccctccctg ccttaaaact tgggagagga gcactcaggg ctggccccac aaagggtctc  1285

gtggcctttt tcctcacaca gaagaggtca gcaataatgt cactgtggac ccagtctcac  1345

tcctccaccc cacacactga agcagtagct tctgggccaa aggtcagggt gggcggggggc  1405

ctgggaatac agcctgtgga ggctgcttac tcaacttgtg tcttaattaa aagtgacaga  1465

ggaaacc                                                            1472
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<210> 29
<211> 137

<212> PRT

<213> Homo sapiens

<400> 29

Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
1   5   10   15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
                20   25   30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
            35   40   45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
        50   55   60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65   70   75   80

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
                85   90   95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
                100   105   110

Gly Ala Ala Ala Pro Tyr Pro Ala Ser Gln Pro Pro Tyr Asn Pro Ala
                115   120   125

Tyr Met Asp Ala Pro Lys Ala Ala Leu

130   135

<210> 30

<211> 1788

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(555)

<400> 30

gtgcttcctg tggctgacgt catctggagg agatttgctt tcttttttctc caaaaggggga 60

ggaaattgaa actgagtggc ccacgatggg aagaggggaa agcccagggg tacaggaggc 120

ctctgggtga aggcagaggc taac atg ggg ttc gga gcg acc ttg gcc gtt   171
                              Met Gly Phe Gly Ala Thr Leu Ala Val
                               1   5

ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc ttc   219
Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys Phe
 10   15   20   25

acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt ccg   267
Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg Pro
           30   35   40

```
gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat cct   315
Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr Pro
            45              50              55


cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag ggc   363
Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln Gly
        60              65              70


tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac cca   411
Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr Pro
        75              80              85


atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg gcc   459
Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro Ala
90              95              100             105


tac cac gag acc ctg gct gga gga gca gcc gcg ccc tac ccc gcc agc   507
Tyr His Glu Thr Leu Ala Gly Gly Ala Ala Ala Pro Tyr Pro Ala Ser
            110             115             120


cag cct cct tac aac ccg gcc tac atg gat gcc ccg aag gcg gcc ctc   555
Gln Pro Pro Tyr Asn Pro Ala Tyr Met Asp Ala Pro Lys Ala Ala Leu
            125             130             135


tgagcattcc ctggcctctc tggctgccac ttggttatgt tgtgtgtgtg cgtgagtggt 615


gtgcaggcgc ggttccttac gccccatgtg tgctgtgtgt gtccaggcac ggttccttac 675


gccccatgtg tgctgtgtgt gtcctgcctg tatatgtggc ttcctctgat gctgacaagg 735
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tggggaacaa tccttgccag agtgggctgg gaccagactt tgttctcttc ctcacctgaa 795

attatgcttc ctaaaatctc aagccaaact caaagaatgg ggtggtgggg ggcaccctgt 855

gaggtggccc ctgagaggtg ggggcctctc cagggcacat ctggagttct tctccagctt 915

accctagggt gaccaagtag ggcctgtcac accagggtgg cgcagctttc tgtgtgatgc 975

agatgtgtcc tggtttcggc agcgtagcca gctgctgctt gaggccatgg ctcgtccccg 1035

gagttggggg tacccgttgc agagccaggg acatgatgca ggcgaagctt gggatctggc 1095

caagttggac tttgatcctt tgggcagatg tcccattgct ccctggagcc tgtcatgcct 1155

gttggggatc aggcagcctc ctgatgccag aacacctcag gcagagccct actcagctgt 1215

acctgtctgc ctggactgtc ccctgtcccc gcatctcccc tgggaccagc tggagggcca 1275

catgcacaca cagcctagct gcccccaggg agctctgctg cccttgctgg ccctgccctt 1335

cccacaggtg agcagggctc ctgtccacca gcacactcag ttctcttccc tgcagtgttt 1395

tcattttatt ttagccaaac attttgcctg ttttctgttt caaacatkat agttgatatg 1455

agactgaaac ccctgggttg tggagggaaa ttggctcaga gatggacaac ctggcaactg 1515

tgagtccctg cttcccgaca ccagcctcat ggaatatgca acaactcctg taccccagtc 1575

cacggtgttc tggcagcagg gacacctggg ccaatgggcc atctggacca aaggtggggt 1635

gtggggccct ggatggcagc tctggcccag acatgaatac ctcgtgttcc tcctccctct 1695

attactgttt caccagagct gtcttagctc aaatctgttg tgtttctgag tctagggtct 1755

gtacacttgt ttataataaa tgcaatcgtt tgg 1788

<210> 31

<211> 118

<212> PRT

<213> Homo sapiens

<400> 31

```
Met Gly Phe Gly Ala Thr Leu Ala Val Gly Leu Thr Ile Phe Val Leu
1               5                   10                  15

Ser Val Val Thr Ile Ile Ile Cys Phe Thr Cys Ser Cys Cys Cys Leu
                20                  25                  30

Tyr Lys Thr Cys Arg Arg Pro Arg Pro Val Val Thr Thr Thr Thr Ser
                35                  40                  45

Thr Thr Val Val His Ala Pro Tyr Pro Gln Pro Pro Ser Val Pro Pro
        50                  55                  60

Ser Tyr Pro Gly Pro Ser Tyr Gln Gly Tyr His Thr Met Pro Pro Gln
65                  70                  75                  80
```

Pro Gly Met Pro Ala Ala Pro Tyr Pro Met Gln Tyr Pro Pro Pro Tyr
            85   90   95

Pro Ala Gln Pro Met Gly Pro Pro Ala Tyr His Glu Thr Leu Ala Gly
          100   105   110

Glu Cys Pro Cys Gln Leu
          115

<210> 32

<211> 1908

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(444)

<400> 32

ggggggaggaa attgaaactg agtggcccac gatgggaaga ggggaaagcc caggggtaca 60

ggaggcctct gggtgaaggc agaggctaac atg ggg ttc gga gcg acc ttg gcc 114
                                      Met Gly Phe Gly Ala Thr Leu Ala
                                        1   5

gtt ggc ctg acc atc ttt gtg ctg tct gtc gtc act atc atc atc tgc 162
Val Gly Leu Thr Ile Phe Val Leu Ser Val Val Thr Ile Ile Ile Cys

```
         10                    15                    20

ttc acc tgc tcc tgc tgc tgc ctt tac aag acg tgc cgc cga cca cgt    210
Phe Thr Cys Ser Cys Cys Cys Leu Tyr Lys Thr Cys Arg Arg Pro Arg
 25                    30                    35                    40


ccg gtt gtc acc acc acc aca tcc acc act gtg gtg cat gcc cct tat    258
Pro Val Val Thr Thr Thr Thr Ser Thr Thr Val Val His Ala Pro Tyr
                       45                    50                    55


cct cag cct cca agt gtg ccg ccc agc tac cct gga cca agc tac cag    306
Pro Gln Pro Pro Ser Val Pro Pro Ser Tyr Pro Gly Pro Ser Tyr Gln
                       60                    65                    70


ggc tac cac acc atg ccg cct cag cca ggg atg cca gca gca ccc tac    354
Gly Tyr His Thr Met Pro Pro Gln Pro Gly Met Pro Ala Ala Pro Tyr
                       75                    80                    85


cca atg cag tac cca cca cct tac cca gcc cag ccc atg ggc cca ccg    402
Pro Met Gln Tyr Pro Pro Pro Tyr Pro Ala Gln Pro Met Gly Pro Pro
                       90                    95                    100


gcc tac cac gag acc ctg gct ggt gag tgc ccc tgc caa ctc            444
Ala Tyr His Glu Thr Leu Ala Gly Glu Cys Pro Cys Gln Leu
105                    110                    115


tagccctgcc cgacttcccg agtctctgcc agcatccctc gggcacccat cccaaactac    504


atcactcaac aggcctctgc ccctttctgc ttgcctgcca ctcacacggc agcccaccat    564
```

出証特２００２−３０３２９３５

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gctcacagcc aaccagggtc ctctctgctt tcaggaggag cagccgcgcc ctaccccgcc 624

agccagcctc cttacaaccc ggcctacatg gatgccccga aggcggccct ctgagcattc 684

cctggcctct ctggctgcca cttggttatg ttgtgtgtgt gcgtgagtgg tgtgcaggcg 744

cggttcctta cgccccatgt gtgctgtgtg tgtccaggca cggttcctta cgccccatgt 804

gtgctgtgtg tgtcctgcct gtatatgtgg cttcctctga tgctgacaag gtggggaaca 864

atccttgcca gagtgggctg ggaccagact ttgttctctt cctcacctga aattatgctt 924

cctaaaatct caagccaaac tcaaagaatg gggtggtggg gggcaccctg tgaggtggcc 984

cctgagaggt gggggcctct ccagggcaca tctggagttc ttctccagct taccctaggg 1044

tgaccaagta gggcctgtca caccagggtg gcgcagcttt ctgtgtgatg cagatgtgtc 1104

ctggtttcgg cagcgtagcc agctgctgct tgaggccatg gctcgtcccc ggagttgggg 1164

gtacccgttg cagagccagg gacatgatgc aggcgaagct tgggatctgg ccaagttgga 1224

ctttgatcct ttgggcagat gtcccattgc tccctggagc ctgtcatgcc tgttggggat 1284

caggcagcct cctgatgcca gaacacctca ggcagagccc tactcagctg tacctgtctg 1344

cctggactgt cccctgtccc cgcatctccc ctgggaccag ctggagggcc acatgcacac 1404
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acagcctagc tgcccccagg gagctctgct gcccttgctg gccctgccct tcccacaggt 1464

gagcagggct cctgtccacc agcacactca gttctcttcc ctgcagtgtt ttcattttat 1524

tttagccaaa cattttgcct gttttctgtt tcaaacatga tagttgatat gagactgaaa 1584

cccctggggtt gtggagggaa attggctcag agatggacaa cctggcaact gtgagtccct 1644

gcttcccgac accagcctca tggaatatgc aacaactcct gtaccccagt ccacggtgtt 1704

ctggcagcag ggacacctgg gccaatgggc catctggacc aaaggtgggg tgtggggccc 1764

tggatggcag ctctggccca gacatgaata cctcgtgttc ctcctccctc tattactgtt 1824

tcaccagagc tgtcttagct caaatctgtt gtgtttctga gtctagggtc tgtacacttg 1884

tttataataa atgcaatcgt ttgg 1908

<210> 33

<211> 168

<212> PRT

<213> Homo sapiens

<400> 33

Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln

  1   5   10   15

Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro Gln Ala

                    20   25   30

Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr Arg Pro
          35   40   45

Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser Ala Ala
       50   55   60

Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val Ala Val
    65   70   75   80

Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val Gly Pro
                85   90   95

Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr Asp Ala
              100   105   110

Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro Pro Pro
        115   120   125

Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met Gln Gly
      130   135   140

Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met Gly Gly
145   150   155   160

Ser Asp Gly Gly Tyr Thr Ile Trp
                165

<210> 34

<211> 1897

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(573)

<400> 34

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gcaaccacc atg aac agc aaa ggt caa tat cca aca cag cca acc tac cct 111
         Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro
         1   5   10

gtg cag cct cct ggg aat cca gta tac cct cag acc ttg cat ctt cct 159
Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr Leu His Leu Pro
 15   20   25   30

cag gct cca ccc tat acc gat gct cca cct gcc tac tca gag ctc tat 207
Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr Ser Glu Leu Tyr
           35   40   45

cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc ccc acc atg tca 255
Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val Pro Thr Met Ser
        50   55   60

gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg gcc cag tct gtg   303
Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met Ala Gln Ser Val
          65   70   75

gct gtt ggg cct tta ggt tcc aca atc ccc atg gct tat tat cca gtc   351
Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala Tyr Tyr Pro Val
          80   85   90

ggt ccc atc tat cca cct ggc tcc aca gtg ctg gtg gaa gga ggg tat   399
Gly Pro Ile Tyr Pro Pro Gly Ser Thr Val Leu Val Glu Gly Gly Tyr
95   100   105   110

gat gca ggt gcc aga ttt gga gct ggg gct act gct ggc aac att cct   447
Asp Ala Gly Ala Arg Phe Gly Ala Gly Ala Thr Ala Gly Asn Ile Pro
               115   120   125

cct cca cct cct gga tgc cct ccc aat gct gct cag ctt gca gtc atg   495
Pro Pro Pro Pro Gly Cys Pro Pro Asn Ala Ala Gln Leu Ala Val Met
               130   135   140

cag gga gcc aac gtc ctc gta act cag cgg aag ggg aac ttc ttc atg   543
Gln Gly Ala Asn Val Leu Val Thr Gln Arg Lys Gly Asn Phe Phe Met
               145   150   155

ggt ggt tca gat ggt ggc tac acc atc tgg tgaggaacca aggccacctc   593
Gly Gly Ser Asp Gly Gly Tyr Thr Ile Trp
               160   165

tgtgccggga aagacatcac ataccttcag cacttctcac aatgtaactg ctttagtcat 653

```
attaacctga agttgcagtt tagacacatg ttgttggggt gtctttctgg tgcccaaact 713

ttcaggcact tttcaaattt aataaggaac catgtaatgg tagcagtacc tccctaaagc 773

attttgaggt aggggaggta tccattcata aaatgaatgt gggtgaagcc gccctaagga 833

ttttccttta atttctctgg agtaatactg taccatactg gtctttgctt ttagtaataa 893

aacatcaaat taggtttgga gggaactttg atcttcctaa gaattaaagt tgccaaatta 953

ttctgattgg tctttaatct cctttaagtc tttgatatat attacttgtt ataaatggaa 1013

cgcattagtt gtctgccttt tcctttccat cccttgcccc acccatccca tctccaaccc 1073

tagtcttcca tttcctcccg ccagtctcca ttgaatcaat ggtgcaggac agaaagccag 1133

tcagactaat ttccttcttt cctcgcactt ctccccactc gtcatctttt aactagtgtt 1193

tcacaaggat cctctgaaac cctctctgtg ccccaagtac agatgccatt acttctgctt 1253

tcgtatctcc tcaggcaaaa gtggagggtg ccttatgggc cctcctcata ggttgtctct 1313

gcatacacga acctaaccca aatttgcttt ggtgccagaa aaactgagct atgtttgaac 1373

aaagatgtcg tgcaaactgt actgtgaaca acagttggtt taaaatatga ggggcaagga 1433

ggaggatgca tttcaaaagc ttgattgatg tgttcagagc taaattaaga ggagttttca 1493
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```
gatcaaaaac tggttaccat tttttgtcag agtgtctgat gcggccactc attcggctcc 1553

ccagaattcc tagactgggt taatagggtc atattgtgaa tgtctcacta caaaatgact 1613

tgagtccagt gaaatctcat tagggtttaa gaatatttca gggatcctta atgttttgat 1673

ttttgttttc tgaaattgga ttttatttta ttttatctta taatttcagt tcatctaaat 1733

tgtgtgttct gtacatgtga tgtttgactg taccattgac tgttatggaa gttcagcgtt 1793

gtatgtctct ctctacactg tggtgcactt aacttgtgga atttttatac taaaaatgta 1853

gaataaagac tattttgaag atttgaataa agtgatgaag ttgc              1897
```


<210> 35

<211> 455

<212> PRT

<213> Homo sapiens

<400> 35

Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu
 1   5   10   15

Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp
                20   25   30

Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe
                35   40   45

```
Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly
     50              55              60

Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys
 65              70              75              80

Val Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr
                 85              90              95

Phe Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe
                100             105             110

Ser Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly
                115             120             125

Asp Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu
    130             135             140

Gln Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu
145             150             155             160

Leu Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr
                165             170             175

Phe Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg
                180             185             190

Leu Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala
```

```
                195                   200                   205
```

```
Met Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro
        210                   215                   220
```

```
Ser Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly
225                   230                   235                   240
```

```
Ser Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu
                    245                   250                   255
```

```
Leu Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys
                260                   265                   270
```

```
Glu Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe
                275                   280                   285
```

```
Leu Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala
        290                   295                   300
```

```
Thr Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr
305                   310                   315                   320
```

```
Arg Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val
                325                   330                   335
```

```
Lys Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile
                340                   345                   350
```

Val Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr
     355   360   365

Ala Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala
     370   375   380

Gln Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met
  385   390   395   400

Ser Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu
        405   410   415

Leu Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val
     420   425   430

Ser Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala
     435   440   445

Pro Glu Lys Gln Met Ala Pro
     450   455

<210> 36

<211> 1903

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116)..(1480)

<400> 36

agtcccggct gcagcacctg ggagaaggca gaccgtgtga gggggcctgt ggccccagcg 60

tgctgtggcc tcggggagtg ggaagtggag gcaggagcct tccttacact tcgcc atg 118
                                                              Met
                                                               1

agt ttc ctc atc gac tcc agc atc atg att acc tcc cag ata cta ttt 166
Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile Leu Phe
            5   10   15

ttt gga ttt ggg tgg ctt ttc ttc atg cgc caa ttg ttt aaa gac tat 214
Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe Lys Asp Tyr
        20   25   30

gag ata cgt cag tat gtt gta cag gtg atc ttc tcc gtg acg ttt gca 262
Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser Val Thr Phe Ala
        35   40   45

ttt tct tgc acc atg ttt gag ctc atc atc ttt gaa atc tta gga gta 310
Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe Glu Ile Leu Gly Val
50   55   60   65

ttg aat agc agc tcc cgt tat ttt cac tgg aaa atg aac ctg tgt gta 358
Leu Asn Ser Ser Ser Arg Tyr Phe His Trp Lys Met Asn Leu Cys Val
            70   75   80

att ctg ctg atc ctg gtt ttc atg gtg cct ttt tac att ggc tat ttt   406
Ile Leu Leu Ile Leu Val Phe Met Val Pro Phe Tyr Ile Gly Tyr Phe
           85   90   95

att gtg agc aat atc cga cta ctg cat aaa caa cga ctg ctt ttt tcc   454
Ile Val Ser Asn Ile Arg Leu Leu His Lys Gln Arg Leu Leu Phe Ser
          100   105   110

tgt ctc tta tgg ctg acc ttt atg tat ttc ttc tgg aaa cta gga gat   502
Cys Leu Leu Trp Leu Thr Phe Met Tyr Phe Phe Trp Lys Leu Gly Asp
          115   120   125

ccc ttt ccc att ctc agc cca aaa cat ggg atc tta tcc ata gaa cag   550
Pro Phe Pro Ile Leu Ser Pro Lys His Gly Ile Leu Ser Ile Glu Gln
130   135   140   145

ctc atc agc cgg gtt ggt gtg att gga gtg act ctc atg gct ctt ctt   598
Leu Ile Ser Arg Val Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu
          150   155   160

tct gga ttt ggt gct gtc aac tgc cca tac act tac atg tct tac ttc   646
Ser Gly Phe Gly Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe
          165   170   175

ctc agg aat gtg act gac acg gat att cta gcc ctg gaa cgg cga ctg   694
Leu Arg Asn Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu
          180   185   190

ctg caa acc atg gat atg atc ata agc aaa aag aaa agg atg gca atg   742

```
Leu Gln Thr Met Asp Met Ile Ile Ser Lys Lys Lys Arg Met Ala Met
    195                 200                 205
```

```
gca cgg aga aca atg ttc cag aag ggg gaa gtg cat aac aaa cca tca    790
Ala Arg Arg Thr Met Phe Gln Lys Gly Glu Val His Asn Lys Pro Ser
210                 215                 220                 225
```

```
ggt ttc tgg gga atg ata aaa agt gtt acc act tca gca tca gga agt    838
Gly Phe Trp Gly Met Ile Lys Ser Val Thr Thr Ser Ala Ser Gly Ser
                    230                 235                 240
```

```
gaa aat ctt act ctt att caa cag gaa gtg gat gct ttg gaa gaa tta    886
Glu Asn Leu Thr Leu Ile Gln Gln Glu Val Asp Ala Leu Glu Glu Leu
                245                 250                 255
```

```
agc agg cag ctt ttt ctg gaa aca gct gat cta tat gct acc aag gag    934
Ser Arg Gln Leu Phe Leu Glu Thr Ala Asp Leu Tyr Ala Thr Lys Glu
            260                 265                 270
```

```
aga ata gaa tac tcc aaa acc ttc aag ggg aaa tat ttt aat ttt ctt    982
Arg Ile Glu Tyr Ser Lys Thr Phe Lys Gly Lys Tyr Phe Asn Phe Leu
            275                 280                 285
```

```
ggt tac ttt ttc tct att tac tgt gtt tgg aaa att ttc atg gct acc    1030
Gly Tyr Phe Phe Ser Ile Tyr Cys Val Trp Lys Ile Phe Met Ala Thr
290                 295                 300                 305
```

```
atc aat att gtt ttt gat cga gtt ggg aaa acg gat cct gtc aca aga    1078
Ile Asn Ile Val Phe Asp Arg Val Gly Lys Thr Asp Pro Val Thr Arg
```

                    310   315   320

ggc att gag atc act gtg aat tat ctg gga atc caa ttt gat gtg aag   1126
Gly Ile Glu Ile Thr Val Asn Tyr Leu Gly Ile Gln Phe Asp Val Lys
          325   330   335

ttt tgg tcc caa cac att tcc ttc att ctt gtt gga ata atc atc gtc   1174
Phe Trp Ser Gln His Ile Ser Phe Ile Leu Val Gly Ile Ile Ile Val
          340   345   350

aca tcc atc aga gga ttg ctg atc act ctt acc aag ttc ttt tat gcc   1222
Thr Ser Ile Arg Gly Leu Leu Ile Thr Leu Thr Lys Phe Phe Tyr Ala
          355   360   365

atc tct agc agt aag tcc tcc aat gtc att gtc ctg cta tta gca cag   1270
Ile Ser Ser Ser Lys Ser Ser Asn Val Ile Val Leu Leu Leu Ala Gln
370   375   380   385

ata atg ggc atg tac ttt gtc tcc tct gtg ctg ctg atc cga atg agt   1318
Ile Met Gly Met Tyr Phe Val Ser Ser Val Leu Leu Ile Arg Met Ser
                    390   395   400

atg cct tta gaa tac cgc acc ata atc act gaa gtc ctt gga gaa ctg   1366
Met Pro Leu Glu Tyr Arg Thr Ile Ile Thr Glu Val Leu Gly Glu Leu
          405   410   415

cag ttc aac ttc tat cac cgt tgg ttt gat gtg atc ttc ctg gtc agc   1414
Gln Phe Asn Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser
          420   425   430

```
gct ctc tct agc ata ctc ttc ctc tat ttg gct cac aaa cag gca cca   1462
Ala Leu Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro
    435                 440                 445


gag aag caa atg gca cct tgaacttaag cctactacag actgttagag           1510
Glu Lys Gln Met Ala Pro
450                 455
```

```
gccagtggtt tcaaaattta gatataagag gggggaaaaa tggaaccagg gcctgacatt 1570


ttataaacaa acaaaatgct atggtagcat ttttcacctt catagcatac tccttccccg 1630


tcaggtgata ctatgaccat gagtagcatc agccagaaca tgagagggag aactaactca 1690


agacaatact cagcagagag catcccgtgt ggatatgagg ctggtgtaga ggcggagagg 1750


agccaagaaa ctaaaggtga aaaatacact ggaactctgg ggcaagacat gtctatggta 1810


gctgagccaa acacgtagga tttccgtttt aaggttcaca tggaaaaggt tatagctttg 1870


ccttgagatt gactcattaa aatcagagac tgt                              1903
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<210> 37
<211> 322
<212> PRT
<213> Homo sapiens

<400> 37

Met Ser Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser
1   5   10   15

Ser Ser Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala
            20   25   30

Gly Ala Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser
            35   40   45

Val Ala Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile
        50   55   60

Ile Ser Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser
65   70   75   80

His Tyr Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met
                85   90   95

Met Gly Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala
                100   105   110

Ser Leu Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp
                115   120   125

Lys Ser Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu
                130   135   140

Leu Ser Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu

```
   145                  150                  155                  160
```

```
Thr Leu Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val
                165                  170                  175
```

```
Gln Glu His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp
                180                  185                  190
```

```
Met Glu Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe
                195                  200                  205
```

```
Pro Tyr Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr
    210                  215                  220
```

```
Pro Ala Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu
    225                  230                  235                  240
```

```
Ala Glu Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly
                245                  250                  255
```

```
Lys Lys Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg
                260                  265                  270
```

```
Ile Asn Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His
                275                  280                  285
```

```
Gln Ile Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser
    290                  295                  300
```

Ala Ala Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp

305   310   315   320

Phe Gln

<210> 38

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (292)..(1257)

<400> 38

tactgctggc ggctggagcg gagcgcaccg cggcggtggt gcccagagcg gagcgcagct 60

ccctgccccg cccctccccc tcggcctcgc ggcgacggcg gcggtggcgg cttggacgac 120

tcggagagcc gagtgaagac atttccacct ggacacctga ccatgtgcct gccctgagca 180

gcgaggccca ccaggcatct ctgttgtggg cagcagggcc aggtcctggt ctgtggaccc 240

tcggcagttg gcaggctccc tctgcagtgg ggtctgggcc tcggccccac c atg tcg 297

                                                          Met Ser

                                                            1

agc ctc ggc ggt ggc tcc cag gat gcc ggc ggc agt agc agc agc agc   345
Ser Leu Gly Gly Gly Ser Gln Asp Ala Gly Gly Ser Ser Ser Ser Ser
        5   10   15

acc aat ggc agc ggt ggc agt ggc agc agt ggc cca aag gca gga gca   393
Thr Asn Gly Ser Gly Gly Ser Gly Ser Ser Gly Pro Lys Ala Gly Ala
        20   25   30

gca gac aag agt gca gtg gtg gct gcc gcc gca cca gcc tca gtg gca   441
Ala Asp Lys Ser Ala Val Val Ala Ala Ala Ala Pro Ala Ser Val Ala
    35   40   45   50

gat gac aca cca ccc ccc gag cgt cgg aac aag agc ggt atc atc agt   489
Asp Asp Thr Pro Pro Pro Glu Arg Arg Asn Lys Ser Gly Ile Ile Ser
                55   60   65

gag ccc ctc aac aag agc ctg cgc cgc tcc cgc ccg ctc tcc cac tac   537
Glu Pro Leu Asn Lys Ser Leu Arg Arg Ser Arg Pro Leu Ser His Tyr
                70   75   80

tct tct ttt ggc agc agt ggt ggt agt ggc ggt ggc agc atg atg ggc   585
Ser Ser Phe Gly Ser Ser Gly Gly Ser Gly Gly Gly Ser Met Met Gly
        85   90   95

gga gag tct gct gac aag gcc act gcg gct gca gcc gct gcc tcc ctg   633
Gly Glu Ser Ala Asp Lys Ala Thr Ala Ala Ala Ala Ala Ala Ser Leu
        100   105   110

ttg gcc aat ggg cat gac ctg gcg gcg gcc atg gcg gtg gac aaa agc   681

Leu Ala Asn Gly His Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser
115   120   125   130

aac cct acc tca aag cac aaa agt ggt gct gtg gcc agc ctg ctg agc   729
Asn Pro Thr Ser Lys His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser
                135   140   145

aag gca gag cgg gcc acg gag ctg gca gcc gag gga cag ctg acg ctg   777
Lys Ala Glu Arg Ala Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu
                150   155   160

cag cag ttt gcg cag tcc aca gag atg ctg aag cgc gtg gtg cag gag   825
Gln Gln Phe Ala Gln Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu
                165   170   175

cat ctc ccg ctg atg agc gag gcg ggt gct ggc ctg cct gac atg gag   873
His Leu Pro Leu Met Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu
                180   185   190

gct gtg gca ggt gcc gaa gcc ctc aat ggc cag tcc gac ttc ccc tac   921
Ala Val Ala Gly Ala Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr
195   200   205   210

ctg ggc gct ttc ccc atc aac cca ggc ctc ttc att atg acc ccg gca   969
Leu Gly Ala Phe Pro Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala
                215   220   225

ggt gtg ttc ctg gcc gag agc gcg ctg cac atg gcg ggc ctg gct gag   1017
Gly Val Phe Leu Ala Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu

```
              230                    235                    240

tac ccc atg cag gga gag ctg gcc tct gcc atc agc tcc ggc aag aag    1065
Tyr Pro Met Gln Gly Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys
              245                    250                    255


aag cgg aaa cgc tgc ggc atg tgc gcg ccc tgc cgg cgg cgc atc aac    1113
Lys Arg Lys Arg Cys Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn
              260                    265                    270


tgc gag cag tgc agc agt tgt agg aat cga aag act ggc cat cag att    1161
Cys Glu Gln Cys Ser Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile
275                    280                    285                    290


tgc aaa ttc aga aaa tgt gag gaa ctc aaa aag aag cct tcc gct gct    1209
Cys Lys Phe Arg Lys Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala
              295                    300                    305


ctg gag aag gtg atg ctt ccg acg gga gcc gcc ttc cgg tgg ttt cag    1257
Leu Glu Lys Val Met Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
              310                    315                    320


tgacggcggc ggaacccaaa gctgccctct ccgtgcaatg tcactgctcg tgtggtctcc    1317


agcaagggat tcgggcgaag acaaacggat gcacccgtct ttagaaccaa aaatattctc    1377


tcacagattt cattcctgtt tttatatata tattttttgt tgtcgtttta acatctccac    1437


gtccctagca t                                                        1448
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<210> 39

<211> 313

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Gly Gln Pro Gly His Met Pro His Gly Gly Ser Ser Asn Asn
1   5   10   15

Leu Cys His Thr Leu Gly Pro Val His Pro Pro Asp Pro Gln Arg His
                20   25   30

Pro Asn Thr Leu Ser Phe Arg Cys Ser Leu Ala Asp Phe Gln Ile Glu
                35   40   45

Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr Lys Ala Thr Cys
        50   55   60

Leu Leu Asp Arg Lys Thr Val Ala Leu Lys Lys Val Gln Ile Phe Glu
65   70   75   80

Met Met Asp Ala Lys Ala Arg Gln Asp Cys Val Lys Glu Ile Gly Leu
                85   90   95

Leu Lys Gln Leu Asn His Pro Asn Ile Ile Lys Tyr Leu Asp Ser Phe
                100   105   110

Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu Ala Asp Ala Gly
     115   120   125

Asp Leu Ser Gln Met Ile Lys Tyr Phe Lys Lys Gln Lys Arg Leu Ile
    130   135   140

Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu Cys Ser Ala Val
  145   150   155   160

Glu His Met His Ser Arg Arg Val Met His Arg Asp Ile Lys Pro Ala
     165   170   175

Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu Gly Asp Leu Gly
     180   185   190

Leu Gly Arg Phe Phe Ser Ser Glu Thr Thr Ala Ala His Ser Leu Val
     195   200   205

Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His Glu Asn Gly Tyr
   210   215   220

Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu Leu Tyr Glu Met
225   230   235   240

Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met Asn Leu Phe Ser
     245   250   255

Leu Cys Gln Lys Ile Glu Gln Cys Asp Tyr Pro Pro Leu Pro Gly Glu
     260   265   270

```
His Tyr Ser Glu Lys Leu Arg Glu Leu Val Ser Met Cys Ile Cys Pro
        275             280             285


Asp Pro His Gln Arg Pro Asp Ile Gly Tyr Val His Gln Val Ala Lys
        290             295             300


Gln Met His Ile Trp Met Ser Ser Thr
305             310
```

<210> 40

<211> 1597

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (153)..(1091)

<400> 40

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ggcggaaccg agctgacggg cgtgcggccg ctgcgccgca aactcgtgtg ggacgcaccg 60


ctccagccgc ccgcgggcca gcgcaccggt cccccagcgg cagccgagcc cgcccgcgcg 120


ccgttcgtgc cctcgtgagg ctggcatgca gg atg gca gga cag ccc ggc cac   173
                                     Met Ala Gly Gln Pro Gly His
                                     1               5
```

```
atg ccc cat gga ggg agt tcc aac aac ctc tgc cac acc ctg ggg cct    221
Met Pro His Gly Gly Ser Ser Asn Asn Leu Cys His Thr Leu Gly Pro
            10              15              20


gtg cat cct cct gac cca cag agg cat ccc aac acg ctg tct ttt cgc    269
Val His Pro Pro Asp Pro Gln Arg His Pro Asn Thr Leu Ser Phe Arg
        25              30              35


tgc tcg ctg gcg gac ttc cag atc gaa aag aag ata ggc cga gga cag    317
Cys Ser Leu Ala Asp Phe Gln Ile Glu Lys Lys Ile Gly Arg Gly Gln
40              45              50                  55


ttc agc gag gtg tac aag gcc acc tgc ctg ctg gac agg aag aca gtg    365
Phe Ser Glu Val Tyr Lys Ala Thr Cys Leu Leu Asp Arg Lys Thr Val
                60              65              70


gct ctg aag aag gtg cag atc ttt gag atg atg gac gcc aag gcg agg    413
Ala Leu Lys Lys Val Gln Ile Phe Glu Met Met Asp Ala Lys Ala Arg
                75              80              85


cag gac tgt gtc aag gag atc ggc ctc ttg aag caa ctg aac cac cca    461
Gln Asp Cys Val Lys Glu Ile Gly Leu Leu Lys Gln Leu Asn His Pro
                90              95              100


aat atc atc aag tat ttg gac tcg ttt atc gaa gac aac gag ctg aac    509
Asn Ile Ile Lys Tyr Leu Asp Ser Phe Ile Glu Asp Asn Glu Leu Asn
            105             110             115


att gtg ctg gag ttg gct gac gca ggg gac ctc tcg cag atg atc aag    557
```

```
Ile Val Leu Glu Leu Ala Asp Ala Gly Asp Leu Ser Gln Met Ile Lys
120             125             130             135


tac ttt aag aag cag aag cgg ctc atc ccg gag agg aca gta tgg aag   605
Tyr Phe Lys Lys Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys
                140             145             150


tac ttt gtg cag ctg tgc agc gcc gtg gag cac atg cat tca cgc cgg   653
Tyr Phe Val Gln Leu Cys Ser Ala Val Glu His Met His Ser Arg Arg
                155             160             165


gtg atg cac cga gac atc aag cct gcc aac gtg ttc atc aca gcc acg   701
Val Met His Arg Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr
            170             175             180


ggc gtc gtg aag ctc ggt gac ctt ggt ctg ggc cgc ttc ttc agc tct   749
Gly Val Val Lys Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser
    185             190             195


gag acc acc gca gcc cac tcc cta gtg ggg acg ccc tac tac atg tca   797
Glu Thr Thr Ala Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser
200             205             210             215


ccg gag agg atc cat gag aac ggc tac aac ttc aag tcc gac atc tgg   845
Pro Glu Arg Ile His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp
                220             225             230


tcc ttg ggc tgt ctg ctg tac gag atg gca gcc ctc cag agc ccc ttc   893
Ser Leu Gly Cys Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe
```

```
                  235                    240                    245


tat gga gat aag atg aat ctc ttc tcc ctg tgc cag aag atc gag cag    941
Tyr Gly Asp Lys Met Asn Leu Phe Ser Leu Cys Gln Lys Ile Glu Gln
        250                    255                    260


tgt gac tac ccc cca ctc ccc ggg gag cac tac tcc gag aag tta cga    989
Cys Asp Tyr Pro Pro Leu Pro Gly Glu His Tyr Ser Glu Lys Leu Arg
        265                    270                    275


gaa ctg gtc agc atg tgc atc tgc cct gac ccc cac cag aga cct gac    1037
Glu Leu Val Ser Met Cys Ile Cys Pro Asp Pro His Gln Arg Pro Asp
280                    285                    290                    295


atc gga tac gtg cac cag gtg gcc aag cag atg cac atc tgg atg tcc    1085
Ile Gly Tyr Val His Gln Val Ala Lys Gln Met His Ile Trp Met Ser
                  300                    305                    310


agc acc tgagcgtgga tgcaccgtgc cttatcaaag ccagcaccac tttgccttac    1141
Ser Thr


ttgagtcgtc ttctcttcga gtggccacct ggtagcctag aacagctaag accacagggt 1201


tcagcaggtt ccccaaaagg ctgcccagcc ttacagcaga tgctgaaggc agagcagctg 1261


agggaggggc gctggccaca tgtcactgat ggtcagattc caaagtcctt tctttatact 1321


gttgtggaca atctcagctg ggtcaataag ggcaggtggt tcagcgagcc acggcagccc 1381
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出証特2002-3032935

cctgtatctg gattgtaatg tgaatcttta gggtaattcc tccagtgacc tgtcaaggct 1441

tatgctaaca ggagacttgc aggagaccgt gtgatttgtg tagtgagcct ttgaaaatgg 1501

ttagtaccgg gttcagttta gttcttggta tcttttcaat caagctgtgt gcttaattta 1561

ctctgttgta aagggataaa gtggaaatca tttttt   1597

<210> 41

<211> 371

<212> PRT

<213> Homo sapiens

<400> 41

Met Ser His Glu Lys Ser Phe Leu Val Ser Gly Asp Asn Tyr Pro Pro
1   5   10   15

Pro Asn Pro Gly Tyr Pro Gly Gly Pro Gln Pro Pro Met Pro Pro Tyr
                20   25   30

Ala Gln Pro Pro Tyr Pro Gly Ala Pro Tyr Pro Gln Pro Pro Phe Gln
                35   40   45

Pro Ser Pro Tyr Gly Gln Pro Gly Tyr Pro His Gly Pro Ser Pro Tyr
        50   55   60

Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro
65   70   75   80

Gln Gly Pro Tyr Pro Gln Glu Gly Tyr Pro Gln Gly Pro Tyr Pro Gln
     85   90   95

Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Ser Pro Phe Pro Pro Asn
     100   105   110

Pro Tyr Gly Gln Pro Gln Val Phe Pro Gly Gln Asp Pro Asp Ser Pro
     115   120   125

Gln His Gly Asn Tyr Gln Glu Glu Gly Pro Pro Ser Tyr Tyr Asp Asn
    130   135   140

Gln Asp Phe Pro Ala Thr Asn Trp Asp Asp Lys Ser Ile Arg Gln Ala
145   150   155   160

Phe Ile Arg Lys Val Phe Leu Val Leu Thr Leu Gln Leu Ser Val Thr
    165   170   175

Leu Ser Thr Val Ser Val Phe Thr Phe Val Ala Glu Val Lys Gly Phe
    180   185   190

Val Arg Glu Asn Val Trp Thr Tyr Tyr Val Ser Tyr Ala Val Phe Phe
    195   200   205

Ile Ser Leu Ile Val Leu Ser Cys Cys Gly Asp Phe Arg Arg Lys His
    210   215   220

Pro Trp Asn Leu Val Ala Leu Ser Val Leu Thr Ala Ser Leu Ser Tyr

```
         225                 230                 235                 240

Met Val Gly Met Ile Ala Ser Phe Tyr Asn Thr Glu Ala Val Ile Met
                 245                 250                 255

Ala Val Gly Ile Thr Thr Ala Val Cys Phe Thr Val Val Ile Phe Ser
                 260                 265                 270

Met Gln Thr Arg Tyr Asp Phe Thr Ser Cys Met Gly Val Leu Leu Val
                 275                 280                 285

Ser Met Val Val Leu Phe Ile Phe Ala Ile Leu Cys Ile Phe Ile Arg
                 290                 295                 300

Asn Arg Ile Leu Glu Ile Val Tyr Ala Ser Leu Gly Ala Leu Leu Phe
305                 310                 315                 320

Thr Cys Phe Leu Ala Val Asp Thr Gln Leu Leu Leu Gly Asn Lys Gln
                 325                 330                 335

Leu Ser Leu Ser Pro Glu Glu Tyr Val Phe Ala Ala Leu Asn Leu Tyr
                 340                 345                 350

Thr Asp Ile Ile Asn Ile Phe Leu Tyr Ile Leu Thr Ile Ile Gly Arg
                 355                 360                 365

Ala Lys Glu
                 370
```

<210> 42

<211> 1781

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(1203)

<400> 42

attggccatc accgcgcggc cgcgcagcgg acaccgtgcg taccggcctg cggcgcccgg 60

ccaccggggc ggaccgcgga acccgaggcc atg tcc cat gaa aag agt ttt ttg 114
                                          Met Ser His Glu Lys Ser Phe Leu
                                         1   5

gtg tct ggg gac aac tat cct ccc ccc aac cct gga tat ccg ggg ggg 162
Val Ser Gly Asp Asn Tyr Pro Pro Pro Asn Pro Gly Tyr Pro Gly Gly
    10   15   20

ccc cag cca ccc atg ccc ccc tat gct cag cct ccc tac cct ggg gcc 210
Pro Gln Pro Pro Met Pro Pro Tyr Ala Gln Pro Pro Tyr Pro Gly Ala
25   30   35   40

cct tac cca cag ccc cct ttc cag ccc tcc ccc tac ggt cag cca ggg 258
Pro Tyr Pro Gln Pro Pro Phe Gln Pro Ser Pro Tyr Gly Gln Pro Gly
          45   50   55

tac ccc cat ggc ccc agc ccc tac ccc caa ggg ggc tac cca cag ggt   306
Tyr Pro His Gly Pro Ser Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly
             60   65   70

ccc tac ccc caa ggg ggc tac cca cag ggc ccc tac cca caa gag ggc   354
Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr Pro Gln Glu Gly
             75   80   85

tac cca cag ggc ccc tac ccc caa ggg ggc tac ccc cag ggg cca tat   402
Tyr Pro Gln Gly Pro Tyr Pro Gln Gly Gly Tyr Pro Gln Gly Pro Tyr
             90   95   100

ccc cag agc ccc ttc ccc ccc aac ccc tat gga cag cca cag gtc ttc   450
Pro Gln Ser Pro Phe Pro Pro Asn Pro Tyr Gly Gln Pro Gln Val Phe
105   110   115   120

cca gga caa gac cct gac tca ccc cag cat gga aac tac cag gag gag   498
Pro Gly Gln Asp Pro Asp Ser Pro Gln His Gly Asn Tyr Gln Glu Glu
               125   130   135

ggt ccc cca tcc tac tat gac aac cag gac ttc cct gcc acc aac tgg   546
Gly Pro Pro Ser Tyr Tyr Asp Asn Gln Asp Phe Pro Ala Thr Asn Trp
             140   145   150

gat gac aag agc atc cga cag gcc ttc atc cgc aag gtg ttc cta gtg   594
Asp Asp Lys Ser Ile Arg Gln Ala Phe Ile Arg Lys Val Phe Leu Val
             155   160   165

ctg acc ttg cag ctg tcg gtg acc ctg tcc acg gtg tct gtg ttc act   642

Leu Thr Leu Gln Leu Ser Val Thr Leu Ser Thr Val Ser Val Phe Thr
    170   175   180

ttt gtt gcg gag gtg aag ggc ttt gtc cgg gag aat gtc tgg acc tac   690
Phe Val Ala Glu Val Lys Gly Phe Val Arg Glu Asn Val Trp Thr Tyr
    185   190   195   200

tat gtc tcc tat gct gtc ttc ttc atc tct ctc atc gtc ctc agc tgt   738
Tyr Val Ser Tyr Ala Val Phe Phe Ile Ser Leu Ile Val Leu Ser Cys
                    205   210   215

tgt ggg gac ttc cgg cga aag cac ccc tgg aac ctt gtt gca ctg tcg   786
Cys Gly Asp Phe Arg Arg Lys His Pro Trp Asn Leu Val Ala Leu Ser
                220   225   230

gtc ctg acc gcc agc ctg tcg tac atg gtg ggg atg atc gcc agc ttc   834
Val Leu Thr Ala Ser Leu Ser Tyr Met Val Gly Met Ile Ala Ser Phe
            235   240   245

tac aac acc gag gca gtc atc atg gcc gtg ggc atc acc aca gcc gtc   882
Tyr Asn Thr Glu Ala Val Ile Met Ala Val Gly Ile Thr Thr Ala Val
    250   255   260

tgc ttc acc gtc gtc atc ttc tcc atg cag acc cgc tac gac ttc acc   930
Cys Phe Thr Val Val Ile Phe Ser Met Gln Thr Arg Tyr Asp Phe Thr
265   270   275   280

tca tgc atg ggc gtg ctc ctg gtg agc atg gtg gtg ctc ttc atc ttc   978
Ser Cys Met Gly Val Leu Leu Val Ser Met Val Val Leu Phe Ile Phe

```
                285                    290                    295


gcc att ctc tgc atc ttc atc cgg aac cgc atc ctg gag atc gtg tac   1026
Ala Ile Leu Cys Ile Phe Ile Arg Asn Arg Ile Leu Glu Ile Val Tyr
            300                    305                    310


gcc tca ctg ggc gct ctg ctc ttc acc tgc ttc ctc gca gtg gac acc   1074
Ala Ser Leu Gly Ala Leu Leu Phe Thr Cys Phe Leu Ala Val Asp Thr
            315                    320                    325


cag ctg ctg ctg ggg aac aag cag ctg tcc ctg agc cca gaa gag tat   1122
Gln Leu Leu Leu Gly Asn Lys Gln Leu Ser Leu Ser Pro Glu Glu Tyr
        330                    335                    340


gtg ttt gct gcg ctg aac ctg tac aca gac atc atc aac atc ttc ctg   1170
Val Phe Ala Ala Leu Asn Leu Tyr Thr Asp Ile Ile Asn Ile Phe Leu
345                    350                    355                    360


tac atc ctc acc atc att ggc cgc gcc aag gag tagccgagct ccagctcgct 1223
Tyr Ile Leu Thr Ile Ile Gly Arg Ala Lys Glu
                365                    370


gtgcccgctc aggtggcacg gctggcctgg accctgcccc tggcacggca gtgccagctg 1283


tacttcccct ctctcttgtc cccaggcaca gcctagggaa aaggatgcct ctctccaacc 1343


ctcctgtatg tacactgcag atacttccat ttggacccgc tgtggccaca gcatggcccc 1403


tttagtcctc ccgcccccgc caaggggcag caaggccacg tttccgtgcc acctcctgtc 1463
```

tactcattgt tgcatgagcc ctgtctgcca gcccacccca gggactgggg gcagcaccag 1523

gtcccgggga gagggattga gccaagaggt gagggtgcac gtcttccctc ctgtcccagc 1583

tccccagcct ggcgtagagc acccctcccc tccccccac cccctggag tgctgccctc 1643

tggggacatg cggagtgggg gtcttatccc tgtgctgagc cctgagggca gagaggatgg 1703

catgtttcag gggaggggga agccttcctc tcaatttgtt gtcagtgaaa ttccaataaa 1763

tgggatttgc tctctgcc   1781

<210> 43

<211> 393

<212> PRT

<213> Homo sapiens

<400> 43

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala
1   5   10   15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro
                20   25   30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
        35   40   45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
    50   55   60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
    65   70   75   80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
             85   90   95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
           100   105   110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
           115   120   125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
           130   135   140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
    145   150   155   160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
           165   170   175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
           180   185   190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
           195   200   205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
    210   215   220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225   230   235   240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
            245   250   255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
            260   265   270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
        275   280   285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
    290   295   300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305   310   315   320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
            325   330   335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly
            340   345   350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala

```
             355                  360                  365
```

Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu

```
             370                  375              380
```

Leu Val Pro Gly Pro Glu Lys Glu Asn

```
385                  390
```


<210> 44

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 44

agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac 58

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                                                    Met Ser Asp
                                                      1
```


gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg   106

Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro

```
         5                  10                  15
```


cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc   154

Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser

| | 20 | | | 25 | | | 30 | | | 35 | |

```
gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta    202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
                40                  45                  50

gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg    250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
            55                  60                  65

ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg    298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
        70                  75                  80

cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg    346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
    85                  90                  95

tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg    394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100                 105                 110                 115

ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga    442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
                120                 125                 130

gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg    490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
            135                 140                 145
```

```
act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt    538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
        150                 155                 160


gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc    586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
        165                 170                 175


ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac    634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180                 185                 190                 195


atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca    682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200                 205                 210


gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag    730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                215                 220                 225


gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act    778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
                230                 235                 240


gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att    826
Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
                245                 250                 255
```

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc   874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260   265   270   275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg   922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
                280   285   290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat   970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
                295   300   305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg   1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
                310   315   320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt   1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
                325   330   335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag   1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340   345   350   355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg   1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met
                360   365   370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca   1210

Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro
      375   380   385

ggg cca gag aag gag aac tagggcaagt ggctgtgaga ccctagagac   1258
Gly Pro Glu Lys Glu Asn
      390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct 1318

ctgtcataat gctctgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc 1378

tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg 1438

ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt 1498

ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtccccctg ttgtgttcca 1558

tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa 1618

ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct 1678

ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca 1738

atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt 1798

ctgccattct taaccaaggc agccccaagc ctcctgggga ggcagggcaa aaacaggtgc 1858

cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcgggggaag 1918

cttcctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgct 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcagggaa gtacagagtg ggatggtcag gacctgggcc 2158

attgcaacca aaatggggac ttcctgggta gggaggtcac tccctctact cactgagcta 2218

ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

accaccccat taccacagct gcctttgtgt gtttgtgtca ataaaaagcc aaaccctg 2396

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Ser Asp Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala

1   5   10   15

Ser Ser Pro Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro

            20   25   30

Ala Ala Ser Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu
         35   40   45

Arg Cys Leu Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu
         50   55   60

Gln Ser Arg Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr
     65   70   75   80

Leu Arg Leu Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg
                 85   90   95

Gln Gly Leu Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met
             100   105   110

Glu Gly Ala Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg
             115   120   125

Lys Ala Gly Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln
         130   135   140

Glu Glu Val Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala
145   150   155   160

Met Thr Phe Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala
                 165   170   175

Tyr Met Val Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val
             180   185   190

Leu Val His Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu
    195   200   205

Cys Arg Thr Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser
    210   215   220

Lys His Glu Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr
225   230   235   240

His Thr Thr Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly
       245   250   255

Val Asp Ile Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly
       260   265   270

Tyr Asn Leu Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala
       275   280   285

Asn Leu Leu Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr
    290   295   300

Trp Trp Asn Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn
305   310   315   320

Arg Ala Val Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu
       325   330   335

Leu Val Ser Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly

```
         340                345                350

His Ile Lys Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala
     355                360                365


Asp Ala Met Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu
     370                375                380


Leu Val Pro Gly Pro Glu Lys Gln Asn
385                390
```

<210> 46

<211> 2396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(1228)

<400> 46

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agctgtgcac tctccatcca gctgtgcgct ctcgtcggga gtcccagcc atg tcc gac  58
                                                        Met Ser Asp
                                                          1


gag aga gag gta gcc gag gca gcg acc ggg gaa gac gcc tct tcg ccg  106
Glu Arg Glu Val Ala Glu Ala Ala Thr Gly Glu Asp Ala Ser Ser Pro
    5                10                15
```

```
cct ccg aaa acc gag gca gcg agc gac ccc cag cat ccc gcg gcc tcc    154
Pro Pro Lys Thr Glu Ala Ala Ser Asp Pro Gln His Pro Ala Ala Ser
20              25              30              35


gaa ggg gcc gcc gcc gcc gcc gcc tcg ccg cca ctg ctg cgc tgc cta    202
Glu Gly Ala Ala Ala Ala Ala Ala Ser Pro Pro Leu Leu Arg Cys Leu
            40              45              50


gtg ctc acc ggc ttt gga ggc tac gac aag gtg aag ctg cag agc cgg    250
Val Leu Thr Gly Phe Gly Gly Tyr Asp Lys Val Lys Leu Gln Ser Arg
            55              60              65


ccg gca gcg ccc ccg gcc cct ggg ccc ggc cag ctg acg ctg cgt ctg    298
Pro Ala Ala Pro Pro Ala Pro Gly Pro Gly Gln Leu Thr Leu Arg Leu
            70              75              80


cgg gcc tgc ggg ctc aac ttc gca gac ctc atg gct agg cag ggg ctg    346
Arg Ala Cys Gly Leu Asn Phe Ala Asp Leu Met Ala Arg Gln Gly Leu
            85              90              95


tac gac cgt ctc ccg cct ctg cct gtc act ccg ggc atg gag ggc gcg    394
Tyr Asp Arg Leu Pro Pro Leu Pro Val Thr Pro Gly Met Glu Gly Ala
100             105             110             115


ggt gtt gtg atc gca gtg ggc gag gga gtc agc gac cgc aag gca gga    442
Gly Val Val Ile Ala Val Gly Glu Gly Val Ser Asp Arg Lys Ala Gly
            120             125             130
```

出証特２００２－３０３２９３５

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gac cgg gtg atg gtg ttg aac cgg tca ggg atg tgg cag gaa gag gtg    490
Asp Arg Val Met Val Leu Asn Arg Ser Gly Met Trp Gln Glu Glu Val
        135                 140                 145


act gtg ccc tcg gtc cag acc ttc ctg att cct gag gcc atg acc ttt    538
Thr Val Pro Ser Val Gln Thr Phe Leu Ile Pro Glu Ala Met Thr Phe
        150                 155                 160


gag gaa gct gct gcc ttg ctc gtc aat tac att aca gcc tac atg gtc    586
Glu Glu Ala Ala Ala Leu Leu Val Asn Tyr Ile Thr Ala Tyr Met Val
        165                 170                 175


ctc ttt gac ttc ggc aac cta cag cct ggc cac agc gtc ttg gta cac    634
Leu Phe Asp Phe Gly Asn Leu Gln Pro Gly His Ser Val Leu Val His
180                 185                 190                 195


atg gct gca ggg ggt gtg ggt atg gct gcc gtg cag ctg tgc cgt aca    682
Met Ala Ala Gly Gly Val Gly Met Ala Ala Val Gln Leu Cys Arg Thr
                200                 205                 210


gtg gag aat gtg aca gtg ttc gga acg gcc tcg gcc agc aag cac gag    730
Val Glu Asn Val Thr Val Phe Gly Thr Ala Ser Ala Ser Lys His Glu
                215                 220                 225


gca ctg aag gag aat ggg gtc aca cat ccc atc gac tat cac acg act    778
Ala Leu Lys Glu Asn Gly Val Thr His Pro Ile Asp Tyr His Thr Thr
                230                 235                 240


gac tac gtg gat gag atc aag aag att tcc cct aaa gga gtg gac att    826
```

Asp Tyr Val Asp Glu Ile Lys Lys Ile Ser Pro Lys Gly Val Asp Ile
     245   250   255

gtc atg gac cct ctg ggt ggg tca gat act gcc aag ggc tac aac ctc   874
Val Met Asp Pro Leu Gly Gly Ser Asp Thr Ala Lys Gly Tyr Asn Leu
260   265   270   275

ctg aaa ccc atg ggc aaa gtc gtc acc tat gga atg gcc aac ctg ctg   922
Leu Lys Pro Met Gly Lys Val Val Thr Tyr Gly Met Ala Asn Leu Leu
            280   285   290

acg ggc ccc aaa cgg aac ctg atg gcc ctg gcc cgg aca tgg tgg aat   970
Thr Gly Pro Lys Arg Asn Leu Met Ala Leu Ala Arg Thr Trp Trp Asn
            295   300   305

cag ttc agc gtg aca gct ctg cag ctg ctg cag gcc aac cgg gct gtg   1018
Gln Phe Ser Val Thr Ala Leu Gln Leu Leu Gln Ala Asn Arg Ala Val
            310   315   320

tgt ggc ttc cac ctg ggc tac ctg gat ggt gag gtg gag ctg gtc agt   1066
Cys Gly Phe His Leu Gly Tyr Leu Asp Gly Glu Val Glu Leu Val Ser
     325   330   335

ggt gtg gtg gcc cgc ctc ctg gct ctg tac aac cag ggc cac atc aag   1114
Gly Val Val Ala Arg Leu Leu Ala Leu Tyr Asn Gln Gly His Ile Lys
340   345   350   355

ccc cac att gac tca gtc tgg ccc ttc gag aag gtg gct gat gcc atg   1162
Pro His Ile Asp Ser Val Trp Pro Phe Glu Lys Val Ala Asp Ala Met

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                 360                    365                    370

aaa cag atg cag gag aag aag aat gtg ggc aag gtc ctc ctg gtt cca    1210
Lys Gln Met Gln Glu Lys Lys Asn Val Gly Lys Val Leu Leu Val Pro

          375                    380                    385

ggg cca gag aag cag aac tagggcaagt ggctgtgaga ccctagagac         1258
Gly Pro Glu Lys Gln Asn

     390

cagcgaaggg agaagttggg aagctacgtt ctgttggcca ccagacttgc atttcagcct  1318

ctgtcataat gctctgccct ccctcccccg aagttctctg tggtgatgac cgctctcccc  1378

tgcccctccc cgcttcctga cctctgaaga ggttgggaag tgaccatttg gatgtctggg  1438

ccctgccaag gcgacaggga gggtcagagg gaggccggct gcttcctgcc cccacccttt  1498

ccccgggcct gctgtgctgc ttttgtgcca aggttagcca gtcccccctg ttgtgttcca  1558

tgtgctttca cctctgcctc atctttcctc ccgtccctgc cccgccacct ccccaaagaa  1618

ttgaaacgtc agctcaggat atggggccaa tctctgtgag tccagcatgt acctgtctct  1678

ccctagtgtc ccttcagcct gggctgacca gtgcccgcct ctgggcttga ccagttccca  1738

atctcgtcct ctgtccccaa cttcttaagc acaattgggc ttcttccatc tccaggtttt  1798

ctgccattct taaccaaggc agccccaagc ctcctgggga ggcagggcaa aaacaggtgc  1858
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cctcatcgtg gtctgtgcca tgtcccgtct ctatggtggt tgaggagaaa ggcgggggaag 1918

cttcctcagc cttgcagata tgtgtggcat ttactagcca gagctctgaa aggcagtgct 1978

gtctgtttct tgtactggga ccaaagtaaa aatccaagca cattcccctt gcagttaggg 2038

gaggccctac tgccttctca aagcagagag gcagcttatc aaactcagcc caaaactctg 2098

tttacatggg tggggagatg gagcagggaa gtacagagtg ggatggtcag gacctgggcc 2158

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ggattaggga gggttattgc cccaaccatt gcaatgggag gtggagggac aggctcagcc 2278

tcctcattgt ctaaatgagg cctaaatgtg tgaagtgcga tttctgcttt tgtgtacccc 2338

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<210> 47

<211> 138

<212> PRT

<213> Homo sapiens

<400> 47

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　　　　　　　20　　　　　　　　　　25　　　　　　　　　　30

Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe
　　　　　　　35　　　　　　　　　　40　　　　　　　　　　45

Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys
　　　　　　　50　　　　　　　　　　55　　　　　　　　　　60

Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile
65　　　　　　　　　70　　　　　　　　　75　　　　　　　　　80

Gly Trp Pro Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu
　　　　　　　　　85　　　　　　　　　90　　　　　　　　　95

Leu Phe Arg Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val
　　　　　　　100　　　　　　　　　105　　　　　　　　　110

Pro Val Leu Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val
　　　　　　　115　　　　　　　　　120　　　　　　　　　125

Asp Lys Val Gly Glu Ser Asn Asn Met Val
　　　　　　　130　　　　　　　　　135

<210> 48

<211> 2976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(523)

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accctgggct ttccgaggtg ctgtcgccgc tgtccccacc actgcagcc atg atc tcc 118
                                                               Met Ile Ser
                                                                  1

tta acg gac acg cag aaa att gga atg gga tta aca gga ttt gga gtg   166
Leu Thr Asp Thr Gln Lys Ile Gly Met Gly Leu Thr Gly Phe Gly Val
     5   10   15

ttt ttc ctg ttc ttt gga atg att ctc ttt ttt gac aaa gca cta ctg   214
Phe Phe Leu Phe Phe Gly Met Ile Leu Phe Phe Asp Lys Ala Leu Leu
  20   25   30   35

gct att gga aat gtt tta ttt gta gcc ggc ttg gct ttt gta att ggt   262
Ala Ile Gly Asn Val Leu Phe Val Ala Gly Leu Ala Phe Val Ile Gly
           40   45   50

tta gaa aga aca ttc aga ttc ttc ttc caa aaa cat aaa atg aaa gct   310
Leu Glu Arg Thr Phe Arg Phe Phe Phe Gln Lys His Lys Met Lys Ala
         55   60   65

aca ggt ttt ttt ctg ggt ggt gta ttt gta gtc ctt att ggt tgg cct   358

Thr Gly Phe Phe Leu Gly Gly Val Phe Val Val Leu Ile Gly Trp Pro
     70   75   80

ttg ata ggc atg atc ttc gaa att tat gga ttt ttt ctc ttg ttc agg   406
Leu Ile Gly Met Ile Phe Glu Ile Tyr Gly Phe Phe Leu Leu Phe Arg
     85   90   95

ggc ttc ttt cct gtc gtt gtt ggc ttt att aga aga gtg cca gtc ctt   454
Gly Phe Phe Pro Val Val Val Gly Phe Ile Arg Arg Val Pro Val Leu
100   105   110   115

gga tcc ctc cta aat tta cct gga att aga tca ttt gta gat aaa gtt   502
Gly Ser Leu Leu Asn Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val
           120   125   130

gga gaa agc aac aat atg gta taacaacaag tgaatttgaa gactcattta   553
Gly Glu Ser Asn Asn Met Val
          135

aaatattgtg ttatttataa agtcatttga agaatattca gcacaaaatt aaattacatg   613

aaatagcttg taatgttctt tacaggagtt taaaacgtat agcctacaaa gtaccagcag   673

caaattagca aagaagcagt gaaaacaggc ttctactcaa gtgaactaag aagaagtcag   733

caagcaaact gagagaggtg aaatccatgt taatgatgct taagaaactc ttgaaggcta   793

tttgtgttgt ttttccacaa tgtgcgaaac tcagccatcc ttagagaact gtggtgcctg   853

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gtccactgca atggcaaaaa tatttccagt tgcactgtat ctctggaagt gatgcatgaa 973

ttcgattgga ttgtgtcatt ttaaagtatt aaaaccaagg aaaccccaat tttgatgtat 1033

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gtctcattga atagtattat tgaagatact aaatgatgca aaccaaatgg atttttttcca 1393

tgtcatgatg taattttttct ttcttctttc ttttttttaa attttagcag tggcttatta 1453

tttgttttttc ataaattaaa ataacttttg ataatgttta ctttaagaca tgtaacatgt 1513

taaaaggtta aacttatggc tgttttttaaa gggctattca tttaatctga gttttcccctt 1573

attttcagct ttttcctagc atataatagt cattaagcat gacatatcct tcatatgatc 1633

actcatcttg agttaattag aaaatacctg agttcacgtg ctaaagtcat ttcactgtaa 1693

taaactgact atggtttctt aagaacatga cactaaaaaa aaagtggttt ttttccaccg 1753
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ttgctgatta ttagacagta ggaaatagct gttttcttta gttttacaag atgtgacagc 1813

tttagtggta gatgtaggga aacatttcaa cagccatagt actatttgtt ttaccactga 1873

ttgcactgtt ttgttttttt aacagttgca aagctttta atgcataaaa gtataattga 1933

aatctgtggt atttatttac aaacatgtct acaaaaatag attacagctt attttatttt 1993

tagttaaatc tcttaataca cagagaactc ccaatcttgc tcatctaaat aaggaaagac 2053

ttggtgtata gtgtgatggt ttagtcttaa ggattaagac atttttggta cttgcatttg 2113

acttacgatg tatctgtgaa aatgggatga tattgacaaa tggagactcc tacctcaata 2173

gttaatggaa taataagagg ctactgttgt gtctaatgtt cttcaaaaaa gtaatatcct 2233

cacttggaga gtgtcaaata catactttga ggattgactt tatataaggt gccctgtaga 2293

actctgttac acatattttt gacccatatt atttacaatg tcttgataat tctacctttt 2353

tagagcaaga atagtatctg ctaatgtaag ggacatctgt atttaactcc tttgtagaca 2413

tgaatttcta tcaaaatgtt ctttgcactg taacagagat tccttttttc aataatctta 2473

attcaaaagc attattagac ttgaaagggt ttgataatct cccagtcctt agtaaagatt 2533

gagagaggct ggagcagttt tcagtttttaa atgagtctgc agttaatatc aaatgtgagt 2593
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ttgggactgc ctggcaacat ttatatttct tattcagaac ccttgatgag actattttta 2653

aacatactag tctgctgata gaaagcacta tacatcctat tgtttctttc tttccaaaat 2713

cagccttctg tctgtaacaa aaatgtactt tatagagatg gaggaaaagg tctaatacta 2773

catagcctta agtgtttctg tcattgttca agtgtatttt ctgtaacaga aacatatttg 2833

gaatgttttt cttttcccct tataaattgt aattcctgaa atactgctgc tttaaaaagt 2893

cccactgtca gattatatta tctaacaatt gaatattgta aatatacttg tcttacctct 2953

caataaaagg gtacttttct att   2976

<210> 49

<211> 359

<212> PRT

<213> Homo sapiens

<400> 49

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His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln
                20   25   30

Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val
                35   40   45

Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro
　　　　　　50　　　　　　　　　55　　　　　　　　　60

Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met
65　　　　　　　　　70　　　　　　　　　75　　　　　　　　　80

Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile
　　　　　　　　85　　　　　　　　90　　　　　　　　95

Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser
　　　　　　100　　　　　　　　105　　　　　　　　110

Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu
　　　　　　115　　　　　　　　120　　　　　　　　125

His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp
　　　　130　　　　　　　　135　　　　　　　　140

Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg
145　　　　　　　　150　　　　　　　　155　　　　　　　　160

Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His
　　　　　　　　165　　　　　　　　170　　　　　　　　175

Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr
　　　　　　180　　　　　　　　185　　　　　　　　190

Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu

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            195                    200                    205
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Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro
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            210                    215                    220
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Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile
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   225                    230                    235                    240
```

Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser
```
                       245                    250                    255
```

Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser
```
                       260                    265                    270
```

Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe
```
                       275                    280                    285
```

Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His
```
            290                    295                    300
```

Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met
```
   305                    310                    315                    320
```

Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser
```
                       325                    330                    335
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Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser
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                       340                    345                    350
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Arg Ser Thr Thr His Leu Ile

355

<210> 50

<211> 2636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (327)..(1403)

<400> 50

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atgttaatat attggcaaca attattcagt tatttcaagt accattggaa gaggaaggac 120

aacgtggtgg acctatcctt gcaccagagg agattaagac tatttttggt agcatcccag 180

atatctttga tgtacacact aagataaagg atgatcttga agaccttata gttaattggg 240

atgagagcaa aagcattggt gacatttttc tgaaatattc aaaagatttg gtaaaaacct 300

accctccctt tgtaaacttc tttgaa atg agc aag gaa aca att att aaa tgt 353

                                         Met Ser Lys Glu Thr Ile Ile Lys Cys

                                      1   5

gaa aaa cag aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca 401

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Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala
10              15              20              25


aaa cca gaa tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca   449
Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro
                 30              35              40


gta cag agg tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag   497
Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys
                 45              50              55


cat aca gct gat gaa aat cca gac aaa agc act tta gaa aaa gct att   545
His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile
                 60              65              70


gga tca ctg aag gaa gta atg acg cat att aat gag gat aag aga aaa   593
Gly Ser Leu Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys
             75              80              85


aca gaa gct caa aag caa att ttt gat gtt gtt tat gaa gta gat gga   641
Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly
90              95              100             105


tgc cca gct aat ctt tta tct tct cac cga agc tta gta cag cgg gtt   689
Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val
                 110             115             120


gaa aca att tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta   737
Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val
```

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                125                 130                 135

act ctc ttc ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac   785
Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His
        140                 145                 150


aag gtt att ggc act ttt agg agt cct cat ggc caa acc cga ccc cca   833
Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro
        155                 160                 165


gct tct ctt aag cat att cac cta atg cct ctt tct cag att aag aag   881
Ala Ser Leu Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys
170                 175                 180                 185


gta ttg gac ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg   929
Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu
                190                 195                 200


ctt gtg agg cca cca aca gag cag gca aat gtg cta ctc agt ttc cag   977
Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln
        205                 210                 215


atg aca tca gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt   1025
Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys
        220                 225                 230


cga cat gta gct aac acc att tgt aaa gca gat gct gag aat ctt att   1073
Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile
        235                 240                 245
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tat act gct gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac　1121
Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp
250　　　　　　255　　　　　　260　　　　　　265

agt aca ttg agt aga gca tca aga gca ata aaa aag act tca aaa aag　1169
Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys
　　　　　270　　　　　　275　　　　　　280

gtt aca aga gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga　1217
Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg
　　　　　285　　　　　　290　　　　　　295

agg gct ctt atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc　1265
Arg Ala Leu Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser
　　　　　300　　　　　　305　　　　　　310

agc aat gat aag cat gta atg agt cgt ctt tct agc aca tca tca tta　1313
Ser Asn Asp Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu
　　　　　315　　　　　　320　　　　　　325

gca ggt atc cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa　1361
Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu
330　　　　　　335　　　　　　340　　　　　　345

agg aga agt cat acg tta agt aga tct aca act cat ttg ata　1403
Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
　　　　　350　　　　　　355

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cactaaacta  tgctatttga  tttttcttct  tgaaagagta  aggtttacct  gttacatttt  1583

caagttaatt  catgtaaaaa  atgatagtga  ttttgatgta  atttatctct  tgtttgaatc  1643

tgtcattcaa  aggccaataa  tttaagttgc  tatcagctga  tattagtagc  tttgcaaccc  1703

tgatagagta  aataaatttt  atgggcgggt  gccaaatact  gctgtgaatc  tatttgtata  1763

gtatccatga  atgaatttat  ggaaatagat  atttgtgcag  ctcaatttat  gcagagatta  1823

aatgacatca  taatactgga  tgaaaacttg  catagaattc  tgattaaata  gtgggtctgt  1883

ttcacatgtg  cagtttgaag  tatttaaata  accactcctt  tcacagttta  ttttcttctc  1943

aagcgttttc  aagatctagc  atgtggattt  taaaagattt  gccctcatta  acaagaataa  2003

catttaaagg  agattgtttc  aaaatatttt  tgcaaattga  gataaggaca  gaaagattga  2063

gaaacattgt  atattttgca  aaaacaagat  gtttgtagct  gtttcagaga  gagtacggta  2123

tatttatggt  aattttatcc  actagcaaat  cttgatttag  tttgatagtg  tgtggaattt  2183

tattttgaag  gataagacca  tgggaaaatt  gtggtaaaga  ctgtttgtac  ccttcatgaa  2243

ataattctga  agttgccatc  agttttacta  atcttctgtg  aaatgcatag  atatgcgcat  2303
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gttcaacttt ttattgtggt cttataatta aatgtaaaat tgaaaattca tttgctgttt 2363

caaagtgtga tatctttcac aatagccttt ttatagtcag taattcagaa taatcaagtt 2423

catatggata aatgcatttt tatttcctat ttctttaggg agtgctacaa atgtttgtca 2483

cttaaatttc aagtttctgt tttaatagtt aactgactat agattgtttt ctatgccatg 2543

tatgtgccac ttctgagagt agtaaatgac tctttgctac attttaaaag caattgtatt 2603

agtaagaact ttgtaaataa atacctaaaa ccc   2636

<210> 51

<211> 883

<212> PRT

<213> Homo sapiens

<400> 51

Met Ala Glu Asn Ser Val Leu Thr Ser Thr Thr Gly Arg Thr Ser Leu

1   5   10   15

Ala Asp Ser Ser Ile Phe Asp Ser Lys Val Thr Glu Ile Ser Lys Glu

            20   25   30

Asn Leu Leu Ile Gly Ser Thr Ser Tyr Val Glu Glu Glu Met Pro Gln

            35   40   45

Ile Glu Thr Arg Val Ile Leu Val Gln Glu Ala Gly Lys Gln Glu Glu
    50   55   60

Leu Thr Lys Ala Leu Lys Asp Ile Lys Val Gly Phe Val Lys Met Glu
65   70   75   80

Ser Val Glu Glu Phe Glu Gly Leu Asp Ser Pro Glu Phe Glu Asn Val
            85   90   95

Phe Val Val Thr Asp Phe Gln Asp Ser Val Phe Asn Asp Leu Tyr Lys
        100   105   110

Ala Asp Cys Arg Val Ile Gly Pro Pro Val Val Leu Asn Cys Ser Gln
        115   120   125

Lys Gly Glu Pro Leu Pro Phe Ser Cys Arg Pro Leu Tyr Cys Thr Ser
        130   135   140

Met Met Asn Leu Val Leu Cys Phe Thr Gly Phe Arg Lys Lys Glu Glu
145   150   155   160

Leu Val Arg Leu Val Thr Leu Val His His Met Gly Gly Val Ile Arg
        165   170   175

Lys Asp Phe Asn Ser Lys Val Thr His Leu Val Ala Asn Cys Thr Gln
        180   185   190

Gly Glu Lys Phe Arg Val Ala Val Ser Leu Gly Thr Pro Ile Met Lys
        195   200   205

Pro Glu Trp Ile Tyr Lys Ala Trp Glu Arg Arg Asn Glu Gln Asp Phe
210   215   220

Tyr Ala Ala Val Asp Asp Phe Arg Asn Glu Phe Lys Val Pro Pro Phe
225   230   235   240

Gln Asp Cys Ile Phe Ser Phe Leu Gly Phe Ser Asp Glu Glu Lys Thr
245   250   255

Asn Met Glu Glu Met Thr Glu Met Gln Gly Gly Lys Tyr Leu Pro Leu
260   265   270

Gly Asp Glu Arg Cys Thr His Leu Val Val Glu Glu Asn Ile Val Lys
275   280   285

Asp Leu Pro Phe Glu Pro Ser Lys Lys Leu Tyr Val Val Lys Gln Glu
290   295   300

Trp Phe Trp Gly Ser Ile Gln Met Asp Ala Arg Ala Gly Glu Thr Met
305   310   315   320

Tyr Leu Tyr Glu Lys Ala Asn Thr Pro Glu Leu Lys Lys Ser Val Ser
325   330   335

Met Leu Ser Leu Asn Thr Pro Asn Ser Asn Arg Lys Arg Arg Arg Leu
340   345   350

Lys Glu Thr Leu Ala Gln Leu Ser Arg Asp Thr Asp Val Ser Pro Phe

355   360   365

Pro Pro Arg Lys Arg Pro Ser Ala Glu His Ser Leu Ser Ile Gly Ser
370   375   380

Leu Leu Asp Ile Ser Asn Thr Pro Glu Ser Ser Ile Asn Tyr Gly Asp
385   390   395   400

Thr Pro Lys Ser Cys Thr Lys Ser Ser Lys Ser Ser Thr Pro Val Pro
                             405   410   415

Ser Lys Gln Ser Ala Arg Trp Gln Val Ala Lys Glu Leu Tyr Gln Thr
                             420   425   430

Glu Ser Asn Tyr Val Asn Ile Leu Ala Thr Ile Ile Gln Leu Phe Gln
                             435   440   445

Val Pro Leu Glu Glu Glu Gly Gln Arg Gly Gly Pro Ile Leu Ala Pro
                             450   455   460

Glu Glu Ile Lys Thr Ile Phe Gly Ser Ile Pro Asp Ile Phe Asp Val
465   470   475   480

His Thr Lys Ile Lys Asp Asp Leu Glu Asp Leu Ile Val Asn Trp Asp
                             485   490   495

Glu Ser Lys Ser Ile Gly Asp Ile Phe Leu Lys Tyr Ser Lys Asp Leu
                             500   505   510

Val Lys Thr Tyr Pro Pro Phe Val Asn Phe Phe Glu Met Ser Lys Glu
     515   520   525

Thr Ile Ile Lys Cys Glu Lys Gln Lys Pro Arg Phe His Ala Phe Leu
     530   535   540

Lys Ile Asn Gln Ala Lys Pro Glu Cys Gly Arg Gln Ser Leu Val Glu
545   550   555   560

Leu Leu Ile Arg Pro Val Gln Arg Leu Pro Ser Val Ala Leu Leu Leu
     565   570   575

Asn Asp Leu Lys Lys His Thr Ala Asp Glu Asn Pro Asp Lys Ser Thr
     580   585   590

Leu Glu Lys Ala Ile Gly Ser Leu Lys Glu Val Met Thr His Ile Asn
     595   600   605

Glu Asp Lys Arg Lys Thr Glu Ala Gln Lys Gln Ile Phe Asp Val Val
     610   615   620

Tyr Glu Val Asp Gly Cys Pro Ala Asn Leu Leu Ser Ser His Arg Ser
625   630   635   640

Leu Val Gln Arg Val Glu Thr Ile Ser Leu Gly Glu His Pro Cys Asp
     645   650   655

Arg Gly Glu Gln Val Thr Leu Phe Leu Phe Asn Asp Cys Leu Glu Ile
     660   .665   670

Ala Arg Lys Arg His Lys Val Ile Gly Thr Phe Arg Ser Pro His Gly
     675   680   685

Gln Thr Arg Pro Pro Ala Ser Leu Lys His Ile His Leu Met Pro Leu
     690   695   700

Ser Gln Ile Lys Lys Val Leu Asp Ile Arg Glu Thr Glu Asp Cys His
     705   710   715   720

Asn Ala Phe Ala Leu Leu Val Arg Pro Pro Thr Glu Gln Ala Asn Val
            725   730   735

Leu Leu Ser Phe Gln Met Thr Ser Asp Glu Leu Pro Lys Glu Asn Trp
            740   745   750

Leu Lys Met Leu Cys Arg His Val Ala Asn Thr Ile Cys Lys Ala Asp
            755   760   765

Ala Glu Asn Leu Ile Tyr Thr Ala Asp Pro Glu Ser Phe Glu Val Asn
     770   775   780

Thr Lys Asp Met Asp Ser Thr Leu Ser Arg Ala Ser Arg Ala Ile Lys
     785   790   795   800

Lys Thr Ser Lys Lys Val Thr Arg Ala Phe Ser Phe Ser Lys Thr Pro
            805   810   815

Lys Arg Ala Leu Arg Arg Ala Leu Met Thr Ser His Gly Ser Val Glu

```
            820                 825                 830

Gly Arg Ser Pro Ser Ser Asn Asp Lys His Val Met Ser Arg Leu Ser
        835                 840                 845


Ser Thr Ser Ser Leu Ala Gly Ile Pro Ser Pro Ser Leu Val Ser Leu
        850                 855                 860


Pro Ser Phe Phe Glu Arg Arg Ser His Thr Leu Ser Arg Ser Thr Thr
865                 870                 875                 880


His Leu Ile
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<210> 52

<211> 3910

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (29)..(2677)

<400> 52

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agagtgctga tttagaagaa tacaaatc atg gct gaa aat agt gta tta aca     52
                                 Met Ala Glu Asn Ser Val Leu Thr
                                  1               5
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tcc act act ggg agg act agc ttg gca gac tct tcc att ttt gat tct    100
Ser Thr Thr Gly Arg Thr Ser Leu Ala Asp Ser Ser Ile Phe Asp Ser
     10              15               20


aaa gtt act gag att tcc aag gaa aac tta ctt att gga tct act tca    148
Lys Val Thr Glu Ile Ser Lys Glu Asn Leu Leu Ile Gly Ser Thr Ser
 25               30               35               40


tat gta gaa gaa gag atg cct cag att gaa aca aga gtg ata ttg gtt    196
Tyr Val Glu Glu Glu Met Pro Gln Ile Glu Thr Arg Val Ile Leu Val
                 45               50               55


caa gaa gct gga aaa caa gaa gaa ctt aca aaa gcc tta aag gac att    244
Gln Glu Ala Gly Lys Gln Glu Glu Leu Thr Lys Ala Leu Lys Asp Ile
             60               65               70


aaa gtg ggc ttt gta aag atg gag tca gtg gaa gaa ttt gaa ggt ttg    292
Lys Val Gly Phe Val Lys Met Glu Ser Val Glu Glu Phe Glu Gly Leu
             75               80               85


gat tct ccg gaa ttt gaa aat gta ttt gta gtc acg gac ttt cag gat    340
Asp Ser Pro Glu Phe Glu Asn Val Phe Val Val Thr Asp Phe Gln Asp
         90               95              100


tct gtc ttt aat gac ctc tac aag gct gat tgt aga gtt att gga cca    388
Ser Val Phe Asn Asp Leu Tyr Lys Ala Asp Cys Arg Val Ile Gly Pro
105              110              115              120


cca gtt gta tta aat tgt tca caa aaa gga gag cct ttg cca ttt tca    436
```

```
Pro Val Val Leu Asn Cys Ser Gln Lys Gly Glu Pro Leu Pro Phe Ser
            125                 130                 135


tgt cgc ccg ttg tat tgt aca agt atg atg aat cta gta cta tgc ttt   484
Cys Arg Pro Leu Tyr Cys Thr Ser Met Met Asn Leu Val Leu Cys Phe
            140                 145                 150


act gga ttt agg aaa aaa gaa gaa cta gtc agg ttg gtg aca ttg gtc   532
Thr Gly Phe Arg Lys Lys Glu Glu Leu Val Arg Leu Val Thr Leu Val
            155                 160                 165


cat cac atg ggt gga gtt att cga aaa gac ttt aat tca aaa gtt aca   580
His His Met Gly Gly Val Ile Arg Lys Asp Phe Asn Ser Lys Val Thr
        170                 175                 180


cat ttg gtg gca aat tgt aca caa gga gaa aaa ttc agg gtt gct gtg   628
His Leu Val Ala Asn Cys Thr Gln Gly Glu Lys Phe Arg Val Ala Val
185                 190                 195                 200


agt cta ggt act cca att atg aag cca gaa tgg att tat aaa gct tgg   676
Ser Leu Gly Thr Pro Ile Met Lys Pro Glu Trp Ile Tyr Lys Ala Trp
            205                 210                 215


gaa agg cgg aat gaa cag gat ttc tat gca gca gtt gat gac ttt aga   724
Glu Arg Arg Asn Glu Gln Asp Phe Tyr Ala Ala Val Asp Asp Phe Arg
            220                 225                 230


aat gaa ttt aaa gtt cct cca ttt caa gat tgt att ttt agt ttc ctg   772
Asn Glu Phe Lys Val Pro Pro Phe Gln Asp Cys Ile Phe Ser Phe Leu
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235   240   245

gga ttt tca gat gaa gag aaa acc aat atg gaa gaa atg act gaa atg   820
Gly Phe Ser Asp Glu Glu Lys Thr Asn Met Glu Glu Met Thr Glu Met
    250   255   260

caa gga ggt aaa tat tta ccg ctt gga gat gaa aga tgc act cac ctt   868
Gln Gly Gly Lys Tyr Leu Pro Leu Gly Asp Glu Arg Cys Thr His Leu
265   270   275   280

gta gtt gaa gag aat ata gta aaa gat ctt ccc ttt gaa cct tca aag   916
Val Val Glu Glu Asn Ile Val Lys Asp Leu Pro Phe Glu Pro Ser Lys
                285   290   295

aaa ctt tat gtt gtc aag caa gag tgg ttc tgg gga agc att caa atg   964
Lys Leu Tyr Val Val Lys Gln Glu Trp Phe Trp Gly Ser Ile Gln Met
            300   305   310

gat gcc cga gct gga gaa act atg tat tta tat gaa aag gca aat act   1012
Asp Ala Arg Ala Gly Glu Thr Met Tyr Leu Tyr Glu Lys Ala Asn Thr
            315   320   325

cct gag ctc aag aaa tca gtg tca atg ctt tct cta aat acc cct aac   1060
Pro Glu Leu Lys Lys Ser Val Ser Met Leu Ser Leu Asn Thr Pro Asn
            330   335   340

agc aat cgc aaa cga cgt cgt tta aaa gaa aca ctt gct cag ctt tca   1108
Ser Asn Arg Lys Arg Arg Arg Leu Lys Glu Thr Leu Ala Gln Leu Ser
            345   350   355   360

aga gat aca gac gtg tca cca ttt cca ccc cgt aag cgc cca tca gct   1156
Arg Asp Thr Asp Val Ser Pro Phe Pro Pro Arg Lys Arg Pro Ser Ala
              365   370   375

gag cat tcc ctt tcc ata ggg tca ctc cta gat atc tcc aac aca cca   1204
Glu His Ser Leu Ser Ile Gly Ser Leu Leu Asp Ile Ser Asn Thr Pro
              380   385   390

gag tct agc att aac tat gga gac acc cca aag tct tgt act aag tct   1252
Glu Ser Ser Ile Asn Tyr Gly Asp Thr Pro Lys Ser Cys Thr Lys Ser
              395   400   405

tct aaa agc tcc act cca gtt cct tca aag cag tca gca agg tgg caa   1300
Ser Lys Ser Ser Thr Pro Val Pro Ser Lys Gln Ser Ala Arg Trp Gln
             410   415   420

gtt gca aaa gag ctt tat caa act gaa agt aat tat gtt aat ata ttg   1348
Val Ala Lys Glu Leu Tyr Gln Thr Glu Ser Asn Tyr Val Asn Ile Leu
425   430   435   440

gca aca att att cag tta ttt caa gta cca ttg gaa gag gaa gga caa   1396
Ala Thr Ile Ile Gln Leu Phe Gln Val Pro Leu Glu Glu Glu Gly Gln
              445   450   455

cgt ggt gga cct atc ctt gca cca gag gag att aag act att ttt ggt   1444
Arg Gly Gly Pro Ile Leu Ala Pro Glu Glu Ile Lys Thr Ile Phe Gly
              460   465   470

agc atc cca gat atc ttt gat gta cac act aag ata aag gat gat ctt   1492
Ser Ile Pro Asp Ile Phe Asp Val His Thr Lys Ile Lys Asp Asp Leu
            475   480   485

gaa gac ctt ata gtt aat tgg gat gag agc aaa agc att ggt gac att   1540
Glu Asp Leu Ile Val Asn Trp Asp Glu Ser Lys Ser Ile Gly Asp Ile
        490   495   500

ttt ctg aaa tat tca aaa gat ttg gta aaa acc tac cct ccc ttt gta   1588
Phe Leu Lys Tyr Ser Lys Asp Leu Val Lys Thr Tyr Pro Pro Phe Val
505   510   515   520

aac ttc ttt gaa atg agc aag gaa aca att att aaa tgt gaa aaa cag   1636
Asn Phe Phe Glu Met Ser Lys Glu Thr Ile Ile Lys Cys Glu Lys Gln
            525   530   535

aaa cca aga ttt cat gct ttt ctc aag ata aac caa gca aaa cca gaa   1684
Lys Pro Arg Phe His Ala Phe Leu Lys Ile Asn Gln Ala Lys Pro Glu
            540   545   550

tgt gga cgg cag agc ctt gtt gaa ctt ctt atc cga cca gta cag agg   1732
Cys Gly Arg Gln Ser Leu Val Glu Leu Leu Ile Arg Pro Val Gln Arg
        555   560   565

tta ccc agt gtt gca tta ctt tta aat gat ctt aag aag cat aca gct   1780
Leu Pro Ser Val Ala Leu Leu Leu Asn Asp Leu Lys Lys His Thr Ala
        570   575   580

gat gaa aat cca gac aaa agc act tta gaa aaa gct att gga tca ctg   1828

```
Asp Glu Asn Pro Asp Lys Ser Thr Leu Glu Lys Ala Ile Gly Ser Leu
585             590             595             600


aag gaa gta atg acg cat att aat gag gat aag aga aaa aca gaa gct    1876
Lys Glu Val Met Thr His Ile Asn Glu Asp Lys Arg Lys Thr Glu Ala
                605             610             615


caa aag caa att ttt gat gtt gtt tat gaa gta gat gga tgc cca gct    1924
Gln Lys Gln Ile Phe Asp Val Val Tyr Glu Val Asp Gly Cys Pro Ala
                620             625             630


aat ctt tta tct tct cac cga agc tta gta cag cgg gtt gaa aca att    1972
Asn Leu Leu Ser Ser His Arg Ser Leu Val Gln Arg Val Glu Thr Ile
                635             640             645


tct cta ggt gag cac ccc tgt gac aga gga gaa caa gta act ctc ttc    2020
Ser Leu Gly Glu His Pro Cys Asp Arg Gly Glu Gln Val Thr Leu Phe
                650             655             660


ctc ttc aat gat tgc cta gag ata gca aga aaa cgg cac aag gtt att    2068
Leu Phe Asn Asp Cys Leu Glu Ile Ala Arg Lys Arg His Lys Val Ile
665             670             675             680


ggc act ttt agg agt cct cat ggc caa acc cga ccc cca gct tct ctt    2116
Gly Thr Phe Arg Ser Pro His Gly Gln Thr Arg Pro Pro Ala Ser Leu
                685             690             695


aag cat att cac cta atg cct ctt tct cag att aag aag gta ttg gac    2164
Lys His Ile His Leu Met Pro Leu Ser Gln Ile Lys Lys Val Leu Asp
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                700                     705                     710

ata aga gag aca gaa gat tgc cat aat gct ttt gcc ttg ctt gtg agg    2212
Ile Arg Glu Thr Glu Asp Cys His Asn Ala Phe Ala Leu Leu Val Arg
        715                     720                     725


cca cca aca gag cag gca aat gtg cta ctc agt ttc cag atg aca tca    2260
Pro Pro Thr Glu Gln Ala Asn Val Leu Leu Ser Phe Gln Met Thr Ser
        730                     735                     740


gat gaa ctt cca aaa gaa aac tgg cta aag atg ctg tgt cga cat gta    2308
Asp Glu Leu Pro Lys Glu Asn Trp Leu Lys Met Leu Cys Arg His Val
745                     750                     755                     760


gct aac acc att tgt aaa gca gat gct gag aat ctt att tat act gct    2356
Ala Asn Thr Ile Cys Lys Ala Asp Ala Glu Asn Leu Ile Tyr Thr Ala
                765                     770                     775


gat cca gaa tcc ttt gaa gta aat aca aaa gat atg gac agt aca ttg    2404
Asp Pro Glu Ser Phe Glu Val Asn Thr Lys Asp Met Asp Ser Thr Leu
                780                     785                     790


agt aga gca tca aga gca ata aaa aag act tca aaa aag gtt aca aga    2452
Ser Arg Ala Ser Arg Ala Ile Lys Lys Thr Ser Lys Lys Val Thr Arg
                795                     800                     805


gca ttc tct ttc tcc aaa act cca aaa aga gct ctt cga agg gct ctt    2500
Ala Phe Ser Phe Ser Lys Thr Pro Lys Arg Ala Leu Arg Arg Ala Leu
                810                     815                     820
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atg aca tcc cac ggc tca gtg gag gga aga agt cct tcc agc aat gat    2548
Met Thr Ser His Gly Ser Val Glu Gly Arg Ser Pro Ser Ser Asn Asp
825             830             835             840


aag cat gta atg agt cgt ctt tct agc aca tca tca tta gca ggt atc    2596
Lys His Val Met Ser Arg Leu Ser Ser Thr Ser Ser Leu Ala Gly Ile
                845             850             855


cct tct ccc tcc ctt gtc agc ctt cct tcc ttc ttt gaa agg aga agt    2644
Pro Ser Pro Ser Leu Val Ser Leu Pro Ser Phe Phe Glu Arg Arg Ser
                860             865             870


cat acg tta agt aga tct aca act cat ttg ata tgaagcgtta ccaaaatctt 2697
His Thr Leu Ser Arg Ser Thr Thr His Leu Ile
                875             880


aaattataga aatgtataga cacctcatac tcaaataaga aactgactta aatggtactt 2757

gtaattagca cttggtgaaa gctggaagga agataaataa cactaaacta tgctatttga 2817

tttttcttct tgaaagagta aggtttacct gttacatttt caagttaatt catgtaaaaa 2877

atgatagtga ttttgatgta atttatctct tgtttgaatc tgtcattcaa aggccaataa 2937

tttaagttgc tatcagctga tattagtagc tttgcaaccc tgatagagta aataaatttt 2997

atgggcgggt gccaaatact gctgtgaatc tatttgtata gtatccatga atgaatttat 3057
```

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ggaaatagat atttgtgcag ctcaatttat gcagagatta aatgacatca taatactgga 3117

tgaaaacttg catagaattc tgattaaata gtgggtctgt ttcacatgtg cagtttgaag 3177

tatttaaata accactcctt tcacagttta ttttcttctc aagcgttttc aagatctagc 3237

atgtggattt taaaagattt gccctcatta acaagaataa catttaaagg agattgtttc 3297

aaaatatttt tgcaaattga gataaggaca gaaagattga gaaacattgt atatttgca 3357

aaaacaagat gtttgtagct gtttcagaga gagtacggta tatttatggt aattttatcc 3417

actagcaaat cttgatttag tttgatagtg tgtggaattt tattttgaag gataagacca 3477

tgggaaaatt gtggtaaaga ctgtttgtac ccttcatgaa ataattctga agttgccatc 3537

agttttacta atcttctgtg aaatgcatag atatgcgcat gttcaacttt ttattgtggt 3597

cttataatta aatgtaaaat tgaaaattca tttgctgttt caaagtgtga tatctttcac 3657

aatagccttt ttatagtcag taattcagaa taatcaagtt catatggata aatgcatttt 3717

tatttcctat ttctttaggg agtgctacaa atgtttgtca cttaaatttc aagtttctgt 3777

tttaatagtt aactgactat agattgtttt ctatgccatg tatgtgccac ttctgagagt 3837

agtaaatgac tctttgctac attttaaaag caattgtatt agtaagaact ttgtaaataa 3897

atacctaaaa ccc                                                    3910
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<210> 53

<211> 622

<212> PRT

<213> Homo sapiens

<400> 53

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Met Glu Gly Pro Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly
1               5                   10                  15

Pro His Pro Pro Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn
                20                  25                  30

Lys Glu Leu Ala Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser
            35                  40                  45

Ser Asn Cys Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg
        50                  55                  60

Cys Lys Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys
65                  70                  75                  80

Glu Asn Val Ser Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp
                85                  90                  95

Leu Val Lys Phe Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly
                100                 105                 110
```

Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His
   115   120   125

Leu Pro Met Val Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu
   130   135   140

Ile Asp Gly Glu Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln
   145   150   155   160

His Met Pro Ile Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn
           165   170   175

Met Thr Asp Val Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys
           180   185   190

Val Ile Gly Pro Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser
           195   200   205

Leu Asn Val Val Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala
   210   215   220

Val Ala Ala Gly Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly
225   230   235   240

Ser Ser Leu Asp Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met
           245   250   255

Ala Leu Gln Asn Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu
           260   265   270

Ala Lys Met Arg Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln
    275   280   285

Lys Cys Glu Leu Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp
    290   295   300

Ala Ile Gly Tyr Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys
    305   310   315   320

Gly Cys Leu Leu Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg
           325   330   335

Phe Leu Val Gly Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu
           340   345   350

Leu Ser Ser Val Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe
           355   360   365

Pro Asp Leu Ala Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile
    370   375   380

Val Ala Phe Leu Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly
385   390   395   400

Phe Thr Lys Ala Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu
           405   410   415

Ala Glu Thr Gly Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu

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                   420                    425                    430


Ile Arg Lys Pro Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys
        435                    440                    445


Val Ala Arg Tyr Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly
        450                    455                    460


Phe Gly Asn His His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met
465                    470                    475                    480


Val Cys Gly Trp Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His
                   485                    490                    495


Cys Ala Thr Thr Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln
             500                    505                    510


Ile Val Ala Cys Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr
             515                    520                    525


Phe His Phe Ser Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln
             530                    535                    540


Ile Ala Phe Leu Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys
545                    550                    555                    560


Gln Ser Lys His Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr
                   565                    570                    575
```

```
Asn Leu Gly Phe Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys
            580                 585                 590

Phe Gly Leu Val Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr
            595                 600                 605

Met Val Phe His Pro Ala Arg Glu Lys Val Leu Arg Ser Val
            610                 615                 620
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<210> 54

<211> 2426

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)..(1969)

<400> 54

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gctacttgcc tagtagcctc agccgctgtg ggctcctggg gag atg gag ggg ccg  115
                                               Met Glu Gly Pro
                                                 1

ggg ctg ggc tcg cag tgc agg aat cac agc cat ggc ccc cac cct cca  163
Gly Leu Gly Ser Gln Cys Arg Asn His Ser His Gly Pro His Pro Pro
  5                  10                  15                  20
```

```
gga ttt ggt cga tat ggc atc tgt gca cat gaa aac aaa gaa ctt gcc      211
Gly Phe Gly Arg Tyr Gly Ile Cys Ala His Glu Asn Lys Glu Leu Ala
              25                  30                  35


aat gca aga gaa gct ctt cct ctt ata gag gac tct agt aac tgt gac      259
Asn Ala Arg Glu Ala Leu Pro Leu Ile Glu Asp Ser Ser Asn Cys Asp
              40                  45                  50


att gtc aaa gct act caa tac gga att ttt gaa cga tgt aaa gag ttg      307
Ile Val Lys Ala Thr Gln Tyr Gly Ile Phe Glu Arg Cys Lys Glu Leu
              55                  60                  65


gta gaa gca gga tat gat gtc agg caa cca gat aaa gaa aat gtg tcg      355
Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Ser
      70                  75                  80


ctt ctt cat tgg gct gct att aac aac aga ctg gat ctt gta aag ttt      403
Leu Leu His Trp Ala Ala Ile Asn Asn Arg Leu Asp Leu Val Lys Phe
85                  90                  95                  100


tat att tca aaa ggt gct gtt gta gat cag ttg ggt gga gat tta aat      451
Tyr Ile Ser Lys Gly Ala Val Val Asp Gln Leu Gly Gly Asp Leu Asn
              105                 110                 115


tca act cct ctt cac tgg gcc atc cga caa gga cat tta cct atg gtc      499
Ser Thr Pro Leu His Trp Ala Ile Arg Gln Gly His Leu Pro Met Val
              120                 125                 130
```

　　　　　　　　　　　出証特２００２－３０３２９３５

ata tta tta ctc cag cat ggt gca gac ccc act ctt att gat gga gag 547
Ile Leu Leu Leu Gln His Gly Ala Asp Pro Thr Leu Ile Asp Gly Glu
        135   140   145

gga ttc agc agc atc cac ctg gca gta ttg ttt caa cac atg cct att 595
Gly Phe Ser Ser Ile His Leu Ala Val Leu Phe Gln His Met Pro Ile
        150   155   160

ata gca tat ctc atc tca aag gga cag agt gtg aat atg aca gat gta 643
Ile Ala Tyr Leu Ile Ser Lys Gly Gln Ser Val Asn Met Thr Asp Val
165   170   175   180

aat ggg cag aca cct ctc atg tta tca gct cac aaa gta att ggg cca 691
Asn Gly Gln Thr Pro Leu Met Leu Ser Ala His Lys Val Ile Gly Pro
            185   190   195

gaa cca act gga ttt ctt tta aag ttt aat cct tct ctc aat gtg gtt 739
Glu Pro Thr Gly Phe Leu Leu Lys Phe Asn Pro Ser Leu Asn Val Val
            200   205   210

gat aaa ata cac caa aac act cca ctt cac tgg gca gtt gca gca gga 787
Asp Lys Ile His Gln Asn Thr Pro Leu His Trp Ala Val Ala Ala Gly
            215   220   225

aat gtt aat gca gtt gat aag ctt ttg gaa gct ggt tct agc ctg gat 835
Asn Val Asn Ala Val Asp Lys Leu Leu Glu Ala Gly Ser Ser Leu Asp
        230   235   240

atc cag aat gtt aag gga gaa aca cct ctt gat atg gct cta caa aac 883

```
Ile Gln Asn Val Lys Gly Glu Thr Pro Leu Asp Met Ala Leu Gln Asn
245             250             255             260


aaa aat cag ctc att att cat atg cta aaa aca gaa gcc aaa atg aga    931
Lys Asn Gln Leu Ile Ile His Met Leu Lys Thr Glu Ala Lys Met Arg
                265             270             275


gcc aac caa aag ttc aga ctt tgg agg tgg ctg cag aaa tgc gag ctc    979
Ala Asn Gln Lys Phe Arg Leu Trp Arg Trp Leu Gln Lys Cys Glu Leu
                280             285             290


ttc ctg ctg ctg atg ctt tct gtg att acc atg tgg gct att gga tac    1027
Phe Leu Leu Leu Met Leu Ser Val Ile Thr Met Trp Ala Ile Gly Tyr
            295             300             305


ata ttg gac ttc aat tca gat tct tgg ctt tta aaa gga tgt ctt cta    1075
Ile Leu Asp Phe Asn Ser Asp Ser Trp Leu Leu Lys Gly Cys Leu Leu
        310             315             320


gta aca ctg ttt ttt ctg aca tct ttg ttt cca agg ttc ttg gtt ggg    1123
Val Thr Leu Phe Phe Leu Thr Ser Leu Phe Pro Arg Phe Leu Val Gly
325             330             335             340


tat aag aac ctt gta tac tta cca aca gcc ttt ctg cta agt tct gtt    1171
Tyr Lys Asn Leu Val Tyr Leu Pro Thr Ala Phe Leu Leu Ser Ser Val
                345             350             355


ttt tgg ata ttt atg act tgg ttc atc tta ttt ttt cct gat tta gca    1219
Phe Trp Ile Phe Met Thr Trp Phe Ile Leu Phe Phe Pro Asp Leu Ala
```

360   365   370

```
gga gcc cct ttc tat ttc agt ttc att ttc agc ata gta gcc ttt cta    1267
Gly Ala Pro Phe Tyr Phe Ser Phe Ile Phe Ser Ile Val Ala Phe Leu
        375                    380                    385
```

```
tac ttt ttc tat aag act tgg gca act gat cca ggc ttc act aag gct    1315
Tyr Phe Phe Tyr Lys Thr Trp Ala Thr Asp Pro Gly Phe Thr Lys Ala
    390                    395                    400
```

```
tct gaa gaa gaa aag aaa gtg aat atc atc acc ctt gca gaa act ggc    1363
Ser Glu Glu Glu Lys Lys Val Asn Ile Ile Thr Leu Ala Glu Thr Gly
405                    410                    415                    420
```

```
tct ctg gac ttc aga aca ttt tgt aca tca tgt ctt ata agg aag cca    1411
Ser Leu Asp Phe Arg Thr Phe Cys Thr Ser Cys Leu Ile Arg Lys Pro
                425                    430                    435
```

```
tta agg tca ctc cac tgc cat gta tgc aac tgc tgt gtg gct cga tat    1459
Leu Arg Ser Leu His Cys His Val Cys Asn Cys Cys Val Ala Arg Tyr
                440                    445                    450
```

```
gat caa cac tgc ctg tgg act gga cgg tgc ata ggt ttt ggc aac cat    1507
Asp Gln His Cys Leu Trp Thr Gly Arg Cys Ile Gly Phe Gly Asn His
                455                    460                    465
```

```
cac tat tac ata ttc ttc ttg ttt ttc ctt tcc atg gta tgt ggc tgg    1555
His Tyr Tyr Ile Phe Phe Leu Phe Phe Leu Ser Met Val Cys Gly Trp
                470                    475                    480
```

att ata tat gga tct ttc atc tat ttg tcc agt cat tgt gcc aca aca　1603
Ile Ile Tyr Gly Ser Phe Ile Tyr Leu Ser Ser His Cys Ala Thr Thr
485　　　　　　　　490　　　　　　　495　　　　　　　　500

ttc aaa gaa gat gga tta tgg act tac ctc aat cag att gtg gcc tgt　1651
Phe Lys Glu Asp Gly Leu Trp Thr Tyr Leu Asn Gln Ile Val Ala Cys
　　　　　　　　505　　　　　　　510　　　　　　　　515

tcc cct tgg gtt tta tat atc ttg atg cta gca act ttc cat ttc tca　1699
Ser Pro Trp Val Leu Tyr Ile Leu Met Leu Ala Thr Phe His Phe Ser
　　　　　　520　　　　　　　525　　　　　　　530

tgg tca aca ttt tta tta tta aat caa ctc ttt cag att gcc ttt ctg　1747
Trp Ser Thr Phe Leu Leu Leu Asn Gln Leu Phe Gln Ile Ala Phe Leu
　　　　　535　　　　　　　540　　　　　　545

ggc ctg acc tcc cat gag aga atc agc ctg cag aag cag agc aag cat　1795
Gly Leu Thr Ser His Glu Arg Ile Ser Leu Gln Lys Gln Ser Lys His
　　550　　　　　　　555　　　　　　　560

atg aaa cag acg ttg tcc ctc agg aag aca cca tac aat ctt gga ttc　1843
Met Lys Gln Thr Leu Ser Leu Arg Lys Thr Pro Tyr Asn Leu Gly Phe
565　　　　　　　570　　　　　　575　　　　　　　580

atg cag aac ctg gca gat ttc ttt cag tgt ggc tgc ttt ggc ttg gtg　1891
Met Gln Asn Leu Ala Asp Phe Phe Gln Cys Gly Cys Phe Gly Leu Val
　　　　585　　　　　　　590　　　　　　595

```
aag ccc tgt gtg gta gat tgg aca tca cag tac acc atg gtc ttt cac    1939
Lys Pro Cys Val Val Asp Trp Thr Ser Gln Tyr Thr Met Val Phe His
            600             605             610


cca gcc agg gag aag gtt ctt cgc tca gta tgaagaaaag caacccaaaa    1989
Pro Ala Arg Glu Lys Val Leu Arg Ser Val
            615             620
```

```
ctctcaatct gatttgtttt tgtttatgtc gatgccctgt agtttgaaag tgaagtaaag  2049


atttagaatt cacctaagtc caaaggaaaa cacgtggttt ttaaagccat taggtaaaaa  2109


aagttctcaa taaaggcatt acaatttttt aggtttagaa agatggactt ttctgataaa  2169


tcttggcaga catctaaaaa aaaaaccata tttttcacaa gaaaatgcaa gttacttttt  2229


ttggaaataa tactcactga ttatggataa aatggaatat tttcagatac tatattggct  2289


gtttcaaaat agtactattc tttaaacttg taatttttgc taagttattt gtctttgttg  2349


tatctataaa tatgtaaaaa atatttaaat agatgtacct gttttgcttt cacacttaat  2409


aaaaaatttt tttttgt                                                  2426
```

```
<210> 55

<211> 257

<212> PRT

<213> Homo sapiens
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<400> 55

Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
1   5   10   15

Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
            20   25   30

Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
            35   40   45

Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
        50   55   60

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
    65   70   75   80

Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
                85   90   95

Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
                100   105   110

Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly Ala Gly
            115   120   125

Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser Thr Gly
            130   135   140

Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser Leu Gln
145   150   155   160

His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro Gly Gly
                165   170   175

Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu Ala Leu
                180   185   190

Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile Leu Ala
                195   200   205

Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val Ala Tyr
        210   215   220

Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys Leu Leu
225   230   235   240

Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala Thr Asp
                245   250   255

Gly

<210> 56

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (10)..(780)

<400> 56

```
tttcccaag atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag ctg   51
          Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu
           1               5                   10
```

```
atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg ggc   99
Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly
 15              20                  25                  30
```

```
tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc cgg  147
Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg
                35                  40                  45
```

```
aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca gcc  195
Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala
                50                  55                  60
```

```
gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg ttc  243
Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe
                65                  70                  75
```

```
gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc tac  291
Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr
                80                  85                  90
```

```
atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg tac      339
Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr
 95             100             105             110


tcg cgc aca gtt gcc atc atc ggc ggc ttt ctt gtg ttg gcc agc ggt      387
Ser Arg Thr Val Ala Ile Ile Gly Gly Phe Leu Val Leu Ala Ser Gly
                115             120             125


gct ggg gag ctg tac cgc cgg aaa cct cgc agc cgc tcc ctg cag tcc      435
Ala Gly Glu Leu Tyr Arg Arg Lys Pro Arg Ser Arg Ser Leu Gln Ser
            130             135             140


acc ggc cag gtg ttc ctg ggt atc tac ctc atc tgt gtg gcc tac tca      483
Thr Gly Gln Val Phe Leu Gly Ile Tyr Leu Ile Cys Val Ala Tyr Ser
            145             150             155


ctg cag cac agc aag gag gac cgg ctg gcg tat ctg aac cat ctc cca      531
Leu Gln His Ser Lys Glu Asp Arg Leu Ala Tyr Leu Asn His Leu Pro
            160             165             170


gga ggg gag ctg atg atc cag ctg ttc ttc gtg ctg tat ggc atc ctg      579
Gly Gly Glu Leu Met Ile Gln Leu Phe Phe Val Leu Tyr Gly Ile Leu
175             180             185             190


gcc ctg gcc ttt ctg tca ggc tac tac gtg acc ctc gct gcc cag atc      627
Ala Leu Ala Phe Leu Ser Gly Tyr Tyr Val Thr Leu Ala Ala Gln Ile
            195             200             205
```

ctg gct gta ctg ctg ccc cct gtc atg ctg ctc att gat ggc aat gtt　675
Leu Ala Val Leu Leu Pro Pro Val Met Leu Leu Ile Asp Gly Asn Val
　　　　　　　210　　　　　　　　　215　　　　　　　　　220

gct tac tgg cac aac acg cgg cgt gtt gag ttc tgg aac cag atg aag　723
Ala Tyr Trp His Asn Thr Arg Arg Val Glu Phe Trp Asn Gln Met Lys
　　　　　　　225　　　　　　　　　230　　　　　　　　　235

ctc ctt gga gag agt gtg ggc atc ttc gga act gct gtc atc ctg gcc　771
Leu Leu Gly Glu Ser Val Gly Ile Phe Gly Thr Ala Val Ile Leu Ala
　　　　　　　240　　　　　　　　　245　　　　　　　　　250

act gat ggc tgagttttat ggcaagaggc tgagatgggc acagggagcc　　　820
Thr Asp Gly
255

actgagggtc accctgcctt cctccttgct ggcccagctg ctgtttattt atgctttttg 880

gtctgtttgt ttgatctttt gctttttttaa aattgttttt tgcagttaag aggcagctca 940

tttgtccaaa tttctgggct cagcgcttgg gagggcagga gccctggcac taatgctgta 1000

caggtttttt tcctgttagg agagctgagg ccagctgccc actgagtctc ctgtccctga 1060

gaagggagta tggcagggct gggatgcggc tactgagagt gggagagtgg gagacagagg 1120

aaggaagatg gagattggaa gtgagcaaat gtgaaaaatt cctctttgaa cctggcagat 1180

gcagctaggc tctgcagtgc tgtttggaga ctgtgagagg gagtgtgtgt gttgacacat 1240

gtggatcagg cccaggaagg gcacaggggc tgagcactac agaagtcaca tgggttctca 1300

gggtatgcca ggggcagaaa cagtaccggc tctctgtcac tcaccttgag agtagagcag 1360

accctgttct gctctgggct gtgaaggggt ggagcaggca gtggccagct ttgcccttcc 1420

tgctgtctct gtttctagct ccatggttgg cctggtgggg gtggagttcc ctcccaaaca 1480

ccagaccaca cagtcctcca aaaataaaca ttttatatag   1520

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp Ile Gln
1   5   10   15

Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys Asp Lys
                20   25   30

Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln Val Glu
            35   40   45

Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu Arg Phe
        50   55   60

Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp Ser Ile
65   70   75   80

Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met Arg His
                 85   90   95

Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
                 100   105

<210> 58

<211> 1496

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (9)..(329)

<400> 58

ctaccagg atg gct ctc ttc gct ggt ggc aaa ctg cgt gtg cat ctc gac 50
        Met Ala Leu Phe Ala Gly Gly Lys Leu Arg Val His Leu Asp
        1   5   10

atc cag gtt ggg gag cat gcc aac aac tac cct gag att gct gca aaa 98
Ile Gln Val Gly Glu His Ala Asn Asn Tyr Pro Glu Ile Ala Ala Lys
15   20   25   30

gat aag ctg acg gag cta cag ctc cgc gcc cgc cag ttg ctt gat cag　　146
Asp Lys Leu Thr Glu Leu Gln Leu Arg Ala Arg Gln Leu Leu Asp Gln
　　　　　　　35　　　　　　　　　40　　　　　　　　　45

gtg gaa cag att cag aag gag cag gat tac caa agg tat cgt gaa gag　　194
Val Glu Gln Ile Gln Lys Glu Gln Asp Tyr Gln Arg Tyr Arg Glu Glu
　　　　　　　50　　　　　　　　　55　　　　　　　　　60

cgc ttc cga ctg acg agc gag agc acc aac cag agg gtc cta tgg tgg　　242
Arg Phe Arg Leu Thr Ser Glu Ser Thr Asn Gln Arg Val Leu Trp Trp
　　　　65　　　　　　　　　70　　　　　　　　　75

tcc att gct cag act gtc atc ctc atc ctc act ggc atc tgg cag atg　　290
Ser Ile Ala Gln Thr Val Ile Leu Ile Leu Thr Gly Ile Trp Gln Met
　　80　　　　　　　　　85　　　　　　　　　90

cgt cac ctc aag agc ttc ttt gag gcc aag aag ctg gtg tagtgccctc　　339
Arg His Leu Lys Ser Phe Phe Glu Ala Lys Lys Leu Val
　95　　　　　　　　　100　　　　　　　　105

tttgtatgac ccttcctttt tacctcattt atttggtact ttccccacac agtcctttat 399

ccacctggat ttttagggaa aaaaaatgaa aaagaataag tcacattggt tccatggcca 459

caaaccattc agatcagcca cttgctgacc ctggttctta aggacacatg acattagtcc 519

aatctttcaa aatcttgtct tagggcttgt gaggaatcag aactaaccca ggactcagtc 579

ctgcttcttt tgcctcgagt gattttcctc tgttttttcac taaataagca aatgaaaact 639

```
ctctccatta ccttctgctt tctctttgtc cacttacgca gtaggtgact ggcatgtgcc 699

acagagcagg ccctgcctca ctgtctgctg gtcagttctg ggttcactta atggctttgt 759

gaatgtaaat aaggggcagg tcttggccct agaggattga gatgtttttc tatatcttag 819

aactattttt ggataaatta tatattttcc ttcctagtag aagtgttact gcctgtaact 879

agctcaaaat accaatgcag tttctgcatt ctgggttttg tttttctttt tttttttttt 939

ttttttgagt tttgctcttg tcgcccaggc tggagtgcaa tggcgtgatc tcagctcact 999

ggcaacatct gcctcccggg ttcaaatgat tctcctgcct cagtctcctg agtagctggg 1059

attacaggtg cccgccacca cgctcagcta attttgtat ttttagtaga gatggggttt 1119

taccatgttg gccaggctgg tcttagactc ctgacctcag ttgatccacc tgcctcagcc 1179

tctgcattca gtttattcac atatttttgg taactcccat ggcagctcct aggatttcag 1239

cggtctgtgg gccagaaagc aggcaccagg gctgacctca aggccgtatc agagggccaa 1299

gcagagttct tttggatacc tgcttttcat cccacagggc cttagagtca gaggtaaggt 1359

agcaacagag ctagaatggg gcaatgcact cttaccctcc ttctcaactt ttatttaagc 1419

tgtgctaaat gttttcttca agggaaccag atttagttct ttacagaatt ttccagtgaa 1479
```

ataaaacatg ttgtaat   1496

<210> 59

<211> 272

<212> PRT

<213> Homo sapiens

<400> 59

Met Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly
 1   5   10   15

Pro Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp
                20   25   30

Val Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met
            35   40   45

Met Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly
        50   55   60

Ile Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln
65   70   75   80

Gly Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr
                85   90   95

Glu Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr
                100   105   110

Thr Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys
    115   120   125

Val Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg
    130   135   140

Glu Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu
    145   150   155   160

His Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro
            165   170   175

Ser Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val
            180   185   190

Leu Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr
            195   200   205

Tyr Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu
            210   215   220

Met His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln
225   230   235   240

Tyr Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu
            245   250   255

Arg Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu

260   265   270

<210> 60

<211> 1916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (117)..(932)

<400> 60

atggtaacgg ctcggaagcc taggaggctg ggccggaggg aggcggagga accggtgttc 60

gccgccgccg ctgcttcagc ttattccttg tggcctctgc gggtcctgcc tcagcc atg 119

                           Met

                           1

atg atc cac ggc ttc cag agc agc cac cgg gat ttc tgc ttc ggg ccc 167

Met Ile His Gly Phe Gln Ser Ser His Arg Asp Phe Cys Phe Gly Pro

     5   10   15

tgg aag ctg acg gcg tcc aag acc cac atc atg aag tcg gcg gat gtg 215

Trp Lys Leu Thr Ala Ser Lys Thr His Ile Met Lys Ser Ala Asp Val

     20   25   30

gag aaa tta gcc gat gaa tta cat atg cca tct ctc cct gaa atg atg 263

Glu Lys Leu Ala Asp Glu Leu His Met Pro Ser Leu Pro Glu Met Met

```
            35                    40                    45

ttt gga gac aac gtt tta aga atc cag cat ggg tct ggc ttt gga att    311
Phe Gly Asp Asn Val Leu Arg Ile Gln His Gly Ser Gly Phe Gly Ile
50                    55                    60                    65


gag ttc aat gct aca gat gcg tta aga tgt gta aac aac tac caa gga    359
Glu Phe Asn Ala Thr Asp Ala Leu Arg Cys Val Asn Asn Tyr Gln Gly
                    70                    75                    80


atg ctt aaa gtg gcc tgt gct gaa gag tgg caa gaa agc agg acg gag    407
Met Leu Lys Val Ala Cys Ala Glu Glu Trp Gln Glu Ser Arg Thr Glu
                85                    90                    95


ggt gaa cac tcc aaa gag gtt att aaa cca tat gat tgg acc tat aca    455
Gly Glu His Ser Lys Glu Val Ile Lys Pro Tyr Asp Trp Thr Tyr Thr
                100                   105                   110


aca gat tat aag gga acc tta ctt gga gaa tct ctt aag tta aag gtt    503
Thr Asp Tyr Lys Gly Thr Leu Leu Gly Glu Ser Leu Lys Leu Lys Val
                115                   120                   125


gta cct aca aca gat cat ata gat aca gaa aaa ttg aaa gcc aga gaa    551
Val Pro Thr Thr Asp His Ile Asp Thr Glu Lys Leu Lys Ala Arg Glu
130                   135                   140                   145


cag att aag ttt ttt gaa gaa gtt ctc ctt ttt gag gat gaa ctt cat    599
Gln Ile Lys Phe Phe Glu Glu Val Leu Leu Phe Glu Asp Glu Leu His
                150                   155                   160
```

gat cat gga gtt tca agc ctg agt gtg aag att aga gta atg cct tct   647
Asp His Gly Val Ser Ser Leu Ser Val Lys Ile Arg Val Met Pro Ser
            165   170   175

agc ttt ttc ctg ctg ttg cgg ttt ttc ttg aga att gat ggg gtg ctt   695
Ser Phe Phe Leu Leu Leu Arg Phe Phe Leu Arg Ile Asp Gly Val Leu
            180   185   190

atc aga atg aat gac acg aga ctt tac cat gag gct gac aag acc tac   743
Ile Arg Met Asn Asp Thr Arg Leu Tyr His Glu Ala Asp Lys Thr Tyr
         195   200   205

atg tta cga gaa tat acg tca cga gaa agc aaa att tct agt ttg atg   791
Met Leu Arg Glu Tyr Thr Ser Arg Glu Ser Lys Ile Ser Ser Leu Met
210   215   220   225

cat gtt cca cct tcc ctc ttc acg gaa cct aat gaa ata tcc cag tat   839
His Val Pro Pro Ser Leu Phe Thr Glu Pro Asn Glu Ile Ser Gln Tyr
            230   235   240

tta cca ata aag gaa gca gtt tgt gag aag cta ata ttt cca gaa aga   887
Leu Pro Ile Lys Glu Ala Val Cys Glu Lys Leu Ile Phe Pro Glu Arg
            245   250   255

att gat cct aac cca gca gac tca caa aaa agt aca caa gtg gaa   932
Ile Asp Pro Asn Pro Ala Asp Ser Gln Lys Ser Thr Gln Val Glu
            260   265   270

```
taaaatgtga tacaacatat actcactatg gaatctgact ggacaccttg gctatttgta  992

aggggttatt tttattatga gaattaattg ccttgtttat gtacagattt tctgtagcct 1052

taaaggaaaa aaaaataaag atcgttacag gcaggtttca ctcaactgct atttgtactg 1112

tctgtcttca cattcatatt ccagatttat attttctgga gttaaatttg gatgatttct 1172

aaattatcac aaagtgggac ctcagcagta gtgatgtgtg tgtctcatga gcagtgagca 1232

cagtctgcat tcatcatgaa acactatctt ctaccaggag gaggttaatg taaatcacca 1292

aatcccaatg ccttgtgact ttcataggat tcctgatcat gcatgttgat gtactggctc 1352

ttcactttgg gctttctgat gtttattcac acctttggag agttgcaact tgccacatac 1412

gaaattagtc tcatagtgta gtgaacttca accccaaaat tttaaaaatg tatttccccc 1472

cagttttaaa ttgcctttga aatttaaaaa aaaaaattta gacttagtac cagaaccaaa 1532

aatacctaga tttttggaga acttattaca tacatagaaa catgaatatg gtttaccwct 1592

gtgtgtgtgt gtgtgtgtgt gtgtatacag actttttttt ttaacttgtt gattcagatg 1652

tcttggtccc tgaatagtcc tagattactt attttgagaa ttgattgtta aaaattacag 1712

ggaattaaaa taattgcctt tttttttta gagggtaaga gatgggtaga agagtatgcc 1772

tctgaaaatt ttattagttt attcttgtgg agaataccaa gaaaatgtgt atttgcccat 1832
```

tgctaaatat gatatatgcc attttgtatt tatttgtccc aagtgtcttt ttttaagagg 1892

agaataaaca ataaggaatt actg   1916

<210> 61

<211> 219

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Arg Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser
1   5   10   15

Leu Thr Asp Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp
                20   25   30

Lys Lys Ile Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln
        35   40   45

Ile Lys Lys Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys
    50   55   60

Ala Leu Arg Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp
65   70   75   80

Asn Leu Ala Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile
                85   90   95

Gln Ser Leu Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly
    100   105   110

Val Lys Glu Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile
    115   120   125

Glu Asp Leu Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu
    130   135   140

Ile Gln Glu Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu
145   150   155   160

Asp Asp Leu Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala
    165   170   175

Asp Glu Asp Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile
    180   185   190

Pro Glu Gly Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val
    195   200   205

Asp Glu Phe Gly Leu Pro Gln Ile Pro Ala Ser
    210   215

<210> 62

<211> 1362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (49)..(705)

<400> 62

```
gttttctggt tttgctctag tgtttgggtt tcttcgcggc tgctcaag atg aac cga    57
                                                      Met Asn Arg
                                                       1
```

```
ctc ttc ggg aaa gcg aaa ccc aag gct ccg ccg ccc agc ctg act gac    105
Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp
     5                  10                  15
```

```
tgc att ggc acg gtg gac agt aga gca gaa tcc att gac aag aag att    153
Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
20                  25                  30                  35
```

```
tct cga ttg gat gct gag cta gtg aag tat aag gat cag atc aag aag    201
Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
                40                  45                  50
```

```
atg aga gag ggt cct gca aag aat atg gtc aag cag aaa gcc ttg cga    249
Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
                55                  60                  65
```

```
gtt tta aag caa aag agg atg tat gag cag cag cgg gac aat ctt gcc    297
Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
```

```
          70                    75                    80

caa cag tca ttc aac atg gaa caa gcc aat tat acc atc cag tct ttg   345
Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
     85                    90                    95


aag gac acc aag acc acg gtt gat gct atg aaa ctg gga gta aag gaa   393
Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
100                   105                   110                   115


atg aag aag gca tac aag caa gtg aag atc gac cag att gag gat tta   441
Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
              120                   125                   130


caa gac cag cta gag gat atg atg gaa gat gca aat gaa atc caa gaa   489
Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
                   135                   140                   145


gca ctg agt cgc agt tat ggc acc cca gaa ctg gat gaa gat gat tta   537
Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
              150                   155                   160


gaa gca gag ttg gat gca cta ggt gat gag ctt ctg gct gat gaa gac   585
Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
         165                   170                   175


agt tct tat ttg gat gag gca gca tct gca cct gca att cca gaa ggt   633
Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
180                   185                   190                   195
```

gtt ccc act gat aca aaa aac aag gat gga gtt ctg gtg gat gaa ttt   681
Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
        200   205   210

gga ttg cca cag atc cct gct tca tagatttgca tcattcaagc atatcttgta   735
Gly Leu Pro Gln Ile Pro Ala Ser
        215

aaacaaacac atattatggg actaggaaat atttatcttt ccaaatttgc cataacagat   795

ttaggtttct ttcctttctt tgaaggaaag tttaattaca ttgctctttt attttttcca   855

ttaagagact cattgcttgg gaaatgcttt cttcgtacta aaatttgatt cctttttttt   915

cttatgaaaa acgaactcag tttaaaagta tttttagctc gtatgacttg ttttcattca   975

ttaataataa tttgaaataa aactaaggaa atggaatctt aaaagtctat gacagtgtaa   1035

ctctacagtc tcaaaatgac ctgataaatt gataagacaa agatgagatt attggggctg   1095

ttcatattat gattcagaat cattttctat tgtggtatta taggttggtt aaagtgatgg   1155

cctttttgat gggtttttgtt gtgtcttgtg aacaagtcgt tactgtgtcc attattggaa   1215

tggaattatc actactgtat catgagtggg tattttgatt ctatggttcc ctcagtatta   1275

catcttgact tgtaatcaat tatgaatatt tcttgatatt taatgtatag gacatttatt   1335

tatactcaat aaatattttt caaaagg   1362

<210> 63

<211> 622

<212> PRT

<213> Homo sapiens

<400> 63

Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro
1   5   10   15

Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His Tyr Asn His Gly
                20   25   30

Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp Asp Tyr Ser Thr
            35   40   45

Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg
    50   55   60

Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn
65   70   75   80

Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg Ile Asp Leu Val
                85   90   95

Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln Leu Gly Gly Asp
                100   105   110

Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln Gly His Leu Ser
    115   120   125

Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp
    130   135   140

Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln Phe Gly His Thr
    145   150   155   160

Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp Val Asp Met Met
                165   170   175

Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala Tyr Arg Thr His
                180   185   190

Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn Val Ser Val Asn
                195   200   205

Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His Trp Ala Val Leu
    210   215   220

Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn
225   230   235   240

Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys
                245   250   255

Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln Glu Ala Arg Gln

```
                    260                    265                    270

Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp
        275                    280                    285

Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro Phe Leu Val Ile
        290                    295                    300

Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile
305                    310                    315                    320

Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val Gln Phe Leu Ser
                325                    330                    335

Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu Pro Leu Gly Ile
                340                    345                    350

Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp Phe Phe Trp Phe
        355                    360                    365

Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro Phe Leu Ala Asn
        370                    375                    380

Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro
385                    390                    395                    400

Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys Thr Ile Val Glu
                405                    410                    415
```

Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys
        420   425   430

Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly Val Cys Asn Arg
        435   440   445

Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val Gly Asn Cys Val
        450   455   460

Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu
465   470   475   480

Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu
            485   490   495

His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr
        500   505   510

Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met Phe Leu Asn Ser
        515   520   525

Val Phe His Phe Met Trp Val Ala Val Leu Leu Met Cys Gln Met Tyr
        530   535   540

Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg Met Asn Ala Arg
545   550   555   560

Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile Glu Ser Pro Phe
        565   570   575

Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys
        580   585   590

Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr Arg Gln Tyr Thr
        595   600   605

Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln Leu Val
        610   615   620

<210> 64

<211> 2948

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (14)..(1879)

<400> 64

atttaacacc aag atg gcg gac ggc ccg gat gag tac gat acc gaa gcg   49
             Met Ala Asp Gly Pro Asp Glu Tyr Asp Thr Glu Ala
             1   5   10

ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc caa agc cat   97
Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro Gln Ser His
        15   20   25

```
tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act cat att gat    145
Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr His Ile Asp
        30              35              40


gat tac agc aca tgg gac ata gtc aag gct aca caa tat gga ata tat    193
Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr Gly Ile Tyr
        45              50              55              60


gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta cgg caa ccg    241
Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val Arg Gln Pro
                65              70              75


gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc aat aac aga    289
Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile Asn Asn Arg
                80              85              90


ata gat tta gtc aaa tac tat att tcg aaa ggt gct att gtg gat caa    337
Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile Val Asp Gln
                95              100             105


ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc aca aga caa    385
Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala Thr Arg Gln
        110             115             120


ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt gca gat cct    433
Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly Ala Asp Pro
125             130             135             140


tca tta att gat gga gaa gga tgt agc tgt att cat ctg gct gct cag    481
```

Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu Ala Ala Gln
                 145   150   155

ttc gga cat acc tca att gtt gct tat ctc ata gca aaa gga cag gat   529
Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys Gly Gln Asp
               160   165   170

gta gat atg atg gat cag aat gga atg acg cct tta atg tgg gca gca   577
Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met Trp Ala Ala
               175   180   185

tat aga aca cat agt gtg gat cca act aga ttg ctt tta aca ttc aat   625
Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu Thr Phe Asn
             190   195   200

gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act gct ctg cat   673
Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr Ala Leu His
205   210   215   220

tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt ctt ctg gaa   721
Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu Leu Leu Glu
               225   230   235

gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa tca gcg ctt   769
Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu Ser Ala Leu
               240   245   250

gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac cac tta caa   817
Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn His Leu Gln

255   260   265

gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc ctt aga aag   865
Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe Leu Arg Lys
    270   275   280

ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta gga act cct   913
Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu Gly Thr Pro
285   290   295   300

ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta aat att gat   961
Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu Asn Ile Asp
                305   310   315

tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg gct aca gta   1009
Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp Ala Thr Val
                320   325   330

cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat agt gca ttg   1057
Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His Ser Ala Leu
        335   340   345

ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat gtg acg tgg   1105
Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr Val Thr Trp
    350   355   360

ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc cat ctt cca   1153
Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile His Leu Pro
365   370   375   380

```
ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga aaa tct tgg      1201
Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly Lys Ser Trp
            385                 390                 395


aaa tca gat cca ggg att att aaa gca aca gaa gag caa aag aaa aag      1249
Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln Lys Lys Lys
            400                 405                 410


aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc agt ata ttc      1297
Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu Ser Ile Phe
            415                 420                 425


tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa cat tgt ggt      1345
Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys His Cys Gly
            430                 435                 440


gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc cca tgg gtg      1393
Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys Pro Trp Val
445                 450                 455                 460


ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg ggc tac cta      1441
Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met Gly Tyr Leu
                465                 470                 475


ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt tgt ata tct      1489
Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly Cys Ile Ser
            480                 485                 490
```

```
tac tgg gga ctc cac tgt gag acc act tac acc aag gat gga ttt tgg     1537
Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp Gly Phe Trp
        495             500             505


aca tac att act cag att gcc acg tgt tca cct tgg atg ttt tgg atg     1585
Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met Phe Trp Met
        510             515             520


ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta tta ctc atg     1633
Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val Leu Leu Met
525             530             535             540


tgt cag atg tac cag ata tca tgt tta ggt att act aca aat gaa aga     1681
Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr Asn Glu Arg
                545             550             555


atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca acg tct att     1729
Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr Thr Ser Ile
                560             565             570


gaa agc cca ttc aac cat gga tgt gta aga aat att ata gac ttc ttt     1777
Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile Asp Phe Phe
                575             580             585


gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg gac tgg acc     1825
Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val Asp Trp Thr
        590             595             600


agg cag tat aca ata gaa tat gac caa ata tca gga tct ggg tac cag     1873
```

Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser Gly Tyr Gln
605   610   615   620

ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg cctgaaaatt   1929
Leu Val

gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga gcatgctatg 1989

tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa caaaagtaaa 2049

catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa taattttaat 2109

ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct cacagtattt 2169

ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat cagaaatgtt 2229

cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc agtctagtac 2289

gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt attatgtaca 2349

tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc tactgtgatg 2409

ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca atgttttgtt 2469

tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt gtagtaacct 2529

tactctgagg ttttacggtc tgataatgaa gcacttgcat gagtatagta agtcatgttt 2589

ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa tgtatactag 2649

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cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa acagttccat 2709

ttttaagggt taaggtggta ttttcaagaa aaggcagaac aaataatgca aaattctcag 2769

taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata attgtagaca 2829

aaataatggc atttaactaa agatggagca tgatctgtgt acatagcaca tgtgaataaa 2889

agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag tagaatttc 2948
```

<210> 65

<211> 632

<212> PRT

<213> Homo sapiens

<400> 65

```
Met Gln Arg Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp
1               5                   10                  15


Glu Tyr Asp Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu
            20                  25                  30


Ile Lys Pro Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly
        35                  40                  45


Arg Lys Thr His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala
    50                  55                  60
```

```
Thr Gln Tyr Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly
65              70          75              80

Tyr Asp Val Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp
                85              90              95

Ala Ala Ile Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys
            100         105             110

Gly Ala Ile Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu
            115         120             125

His Trp Ala Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met
        130         135             140

Lys Tyr Gly Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys
145             150             155             160

Ile His Leu Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu
                165             170             175

Ile Ala Lys Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr
            180             185             190

Pro Leu Met Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg
            195             200             205

Leu Leu Leu Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His
```

```
            210                 215                 220

Lys Asn Thr Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val
225                 230                 235                 240

Ile Ser Leu Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile
                        245                 250                 255

Lys Gly Glu Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp
                        260                 265                 270

Met Ile Asn His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn
                    275                 280                 285

Pro Ser Phe Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys
                    290                 295                 300

Val Met Leu Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile
305                 310                 315                 320

Ala Asp Leu Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly
                        325                 330                 335

Gly Val Trp Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His
                    340                 345                 350

Ser Met His Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe
                    355                 360                 365
```

Trp Met Tyr Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe
        370   375   380

Leu Phe Ile His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr
385   390   395   400

Asn Phe Gly Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr
                405   410   415

Glu Glu Gln Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser
                420   425   430

Leu Asp Leu Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val
        435   440   445

Arg Ser Lys His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp
        450   455   460

His His Cys Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg
465   470   475   480

Tyr Phe Met Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met
                485   490   495

Ile Tyr Gly Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr
                500   505   510

Thr Lys Asp Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser
                515   520   525

Pro Trp Met Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp
530   535   540

Val Ala Val Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly
545   550   555   560

Ile Thr Thr Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys
565   570   575

Val Thr Thr Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg
580   585   590

Asn Ile Ile Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro
595   600   605

Val Ile Val Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile
610   615   620

Ser Gly Ser Gly Tyr Gln Leu Val
625   630

<210> 66

<211> 4715

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (108)..(2003)

<400> 66

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gaagaaggag gaggaggccc gcgtcgcctc cggcggggct cgcgctcgcc ccgcgctcgc 60


cctccgcctc gcccgagccc cgggagggtg aaacgctttc tcccagc atg cag cgg    116
                                                      Met Gln Arg
                                                        1


gag gag gga ttt aac acc aag atg gcg gac ggc ccg gat gag tac gat    164
Glu Glu Gly Phe Asn Thr Lys Met Ala Asp Gly Pro Asp Glu Tyr Asp
      5                  10                  15


acc gaa gcg ggc tgt gtg ccc ctt ctc cac cca gag gaa atc aaa ccc    212
Thr Glu Ala Gly Cys Val Pro Leu Leu His Pro Glu Glu Ile Lys Pro
 20                  25                  30                  35


caa agc cat tat aac cat gga tat ggt gaa cct ctt gga cgg aaa act    260
Gln Ser His Tyr Asn His Gly Tyr Gly Glu Pro Leu Gly Arg Lys Thr
                     40                  45                  50


cat att gat gat tac agc aca tgg gac ata gtc aag gct aca caa tat    308
His Ile Asp Asp Tyr Ser Thr Trp Asp Ile Val Lys Ala Thr Gln Tyr
                 55                  60                  65


gga ata tat gaa cgc tgt cga gaa ttg gtg gaa gca ggt tat gat gta    356
Gly Ile Tyr Glu Arg Cys Arg Glu Leu Val Glu Ala Gly Tyr Asp Val
             70                  75                  80
```

```
cgg caa ccg gac aaa gaa aat gtt acc ctc ctc cat tgg gct gcc atc     404
Arg Gln Pro Asp Lys Glu Asn Val Thr Leu Leu His Trp Ala Ala Ile
    85              90              95


aat aac aga ata gat tta gtc aaa tac tat att tcg aaa ggt gct att     452
Asn Asn Arg Ile Asp Leu Val Lys Tyr Tyr Ile Ser Lys Gly Ala Ile
100             105             110             115


gtg gat caa ctt gga ggg gac ctg aat tca act cca ttg cac tgg gcc     500
Val Asp Gln Leu Gly Gly Asp Leu Asn Ser Thr Pro Leu His Trp Ala
                120             125             130


aca aga caa ggc cat cta tcc atg gtt gtg caa cta atg aaa tat ggt     548
Thr Arg Gln Gly His Leu Ser Met Val Val Gln Leu Met Lys Tyr Gly
            135             140             145


gca gat cct tca tta att gat gga gaa gga tgt agc tgt att cat ctg     596
Ala Asp Pro Ser Leu Ile Asp Gly Glu Gly Cys Ser Cys Ile His Leu
        150             155             160


gct gct cag ttc gga cat acc tca att gtt gct tat ctc ata gca aaa     644
Ala Ala Gln Phe Gly His Thr Ser Ile Val Ala Tyr Leu Ile Ala Lys
    165             170             175


gga cag gat gta gat atg atg gat cag aat gga atg acg cct tta atg     692
Gly Gln Asp Val Asp Met Met Asp Gln Asn Gly Met Thr Pro Leu Met
180             185             190             195
```

```
tgg gca gca tat aga aca cat agt gtg gat cca act aga ttg ctt tta      740
Trp Ala Ala Tyr Arg Thr His Ser Val Asp Pro Thr Arg Leu Leu Leu
                200                 205                 210


aca ttc aat gtt tca gtt aac ctt ggt gac aag tat cac aaa aac act      788
Thr Phe Asn Val Ser Val Asn Leu Gly Asp Lys Tyr His Lys Asn Thr
                215                 220                 225


gct ctg cat tgg gca gtg cta gca ggg aat acc aca gtc att agc ctt      836
Ala Leu His Trp Ala Val Leu Ala Gly Asn Thr Thr Val Ile Ser Leu
                230                 235                 240


ctt ctg gaa gct gga gct aat gtt gat gcc cag aat atc aag ggc gaa      884
Leu Leu Glu Ala Gly Ala Asn Val Asp Ala Gln Asn Ile Lys Gly Glu
            245                 250                 255


tca gcg ctt gat ttg gca aaa cag aga aaa aat gtg tgg atg atc aac      932
Ser Ala Leu Asp Leu Ala Lys Gln Arg Lys Asn Val Trp Met Ile Asn
260                 265                 270                 275


cac tta caa gag gca agg caa gca aaa gga tat gac aat ccg tcc ttc      980
His Leu Gln Glu Ala Arg Gln Ala Lys Gly Tyr Asp Asn Pro Ser Phe
                280                 285                 290


ctt aga aag ctg aaa gct gat aag gaa ttt cgg cag aaa gta atg tta     1028
Leu Arg Lys Leu Lys Ala Asp Lys Glu Phe Arg Gln Lys Val Met Leu
                295                 300                 305


gga act cct ttc cta gtt att tgg ctg gtt ggg ttt ata gca gac cta     1076
```

Gly Thr Pro Phe Leu Val Ile Trp Leu Val Gly Phe Ile Ala Asp Leu
        310   315   320

aat att gat tct tgg ctc att aaa ggg cta atg tat ggt ggt gtt tgg   1124
Asn Ile Asp Ser Trp Leu Ile Lys Gly Leu Met Tyr Gly Gly Val Trp
        325   330   335

gct aca gta cag ttt ctt tca aaa tcc ttt ttc gat cat tca atg cat   1172
Ala Thr Val Gln Phe Leu Ser Lys Ser Phe Phe Asp His Ser Met His
        340   345   350   355

agt gca ttg ccc ctt ggg ata tat ttg gca acc aaa ttc tgg atg tat   1220
Ser Ala Leu Pro Leu Gly Ile Tyr Leu Ala Thr Lys Phe Trp Met Tyr
                        360   365   370

gtg acg tgg ttc ttc tgg ttt tgg aat gat ctc aac ttt tta ttt atc   1268
Val Thr Trp Phe Phe Trp Phe Trp Asn Asp Leu Asn Phe Leu Phe Ile
                375   380   385

cat ctt cca ttc ctt gcc aat agt gtt gca ctt ttc tac aat ttt gga   1316
His Leu Pro Phe Leu Ala Asn Ser Val Ala Leu Phe Tyr Asn Phe Gly
        390   395   400

aaa tct tgg aaa tca gat cca ggg att att aaa gca aca gaa gag caa   1364
Lys Ser Trp Lys Ser Asp Pro Gly Ile Ile Lys Ala Thr Glu Glu Gln
        405   410   415

aag aaa aag aca ata gtt gaa ctt gca gag aca gga agt ctg gac ctc   1412
Lys Lys Lys Thr Ile Val Glu Leu Ala Glu Thr Gly Ser Leu Asp Leu

```
          420                   425                   430                   435

agt ata ttc tgc agt acc tgt ttg ata cga aaa ccg gtg agg tcc aaa   1460
Ser Ile Phe Cys Ser Thr Cys Leu Ile Arg Lys Pro Val Arg Ser Lys
              440                   445                   450


cat tgt ggt gtg tgc aac cgc tgt ata gca aaa ttt gat cat cat tgc   1508
His Cys Gly Val Cys Asn Arg Cys Ile Ala Lys Phe Asp His His Cys
              455                   460                   465


cca tgg gtg ggt aac tgt gta ggt gca ggc aac cat aga tat ttt atg   1556
Pro Trp Val Gly Asn Cys Val Gly Ala Gly Asn His Arg Tyr Phe Met
              470                   475                   480


ggc tac cta ttc ttc ttg ctt ttt atg atc tgc tgg atg att tat ggt   1604
Gly Tyr Leu Phe Phe Leu Leu Phe Met Ile Cys Trp Met Ile Tyr Gly
              485                   490                   495


tgt ata tct tac tgg gga ctc cac tgt gag acc act tac acc aag gat   1652
Cys Ile Ser Tyr Trp Gly Leu His Cys Glu Thr Thr Tyr Thr Lys Asp
500                   505                   510                   515


gga ttt tgg aca tac att act cag att gcc acg tgt tca cct tgg atg   1700
Gly Phe Trp Thr Tyr Ile Thr Gln Ile Ala Thr Cys Ser Pro Trp Met
              520                   525                   530


ttt tgg atg ttc ctg aac agt gtt ttc cac ttc atg tgg gtg gct gta   1748
Phe Trp Met Phe Leu Asn Ser Val Phe His Phe Met Trp Val Ala Val
              535                   540                   545
```

```
tta ctc atg tgt cag atg tac cag ata tca tgt tta ggt att act aca     1796
Leu Leu Met Cys Gln Met Tyr Gln Ile Ser Cys Leu Gly Ile Thr Thr
        550                 555                 560


aat gaa aga atg aat gcc agg aga tac aag cac ttt aaa gtc aca aca     1844
Asn Glu Arg Met Asn Ala Arg Arg Tyr Lys His Phe Lys Val Thr Thr
        565                 570                 575


acg tct att gaa agc cca ttc aac cat gga tgt gta aga aat att ata     1892
Thr Ser Ile Glu Ser Pro Phe Asn His Gly Cys Val Arg Asn Ile Ile
580                 585                 590                 595


gac ttc ttt gaa ttt cga tgc tgt ggc ctc ttt cgt cct gtt atc gtg     1940
Asp Phe Phe Glu Phe Arg Cys Cys Gly Leu Phe Arg Pro Val Ile Val
            600                 605                 610


gac tgg acc agg cag tat aca ata gaa tat gac caa ata tca gga tct     1988
Asp Trp Thr Arg Gln Tyr Thr Ile Glu Tyr Asp Gln Ile Ser Gly Ser
            615                 620                 625


ggg tac cag ctg gtg tagcgacatc ttatcctatg aagcatattg ctgagtggtg    2043
Gly Tyr Gln Leu Val
            630


cctgaaaatt gtgtctgtcc gtgtctttct cacactcgaa tccacatcct ttgaacaaga  2103


gcatgctatg tgtagggcta atggtgaatt ttacagtctt tttttcaaca cttttattaa  2163
```

```
caaaagtaaa catggacaga acacactgcc atttctggga agagtaaaga tgataaaaaa 2223

taattttaat ggttcttaat gtggaaattc acaacatact caacttttgg gttttgttct 2283

cacagtattt ttcacaaaaa aagggtaaac ttattctatt gacagacatg gtgtactgat 2343

cagaaatgtt cagttttaac taaaactaaa tttatgttat ttggctaaat gttatgatgc 2403

agtctagtac gagtattgca tctaattcca ggagcattgt tttaagttga ttgactagtt 2463

attatgtaca tttcagaatg tacacataaa tactgtgatg aaaatcatgt gattgggatc 2523

tactgtgatg ttgtcttcaa aggcaggaga aaataatgtt cacaataaaa tgtgctaaca 2583

atgttttgtt tctatcagct gttgcaatgc tgatatattt ctagttcagt gaaataattt 2643

gtagtaacct tactctgagg ttttacggtc tgataatgaa gcacttgcat gagtatagta 2703

agtcatgttt ttttgttcaa atttaaaagc cctgctaatt gcatgacaca ccacatagaa 2763

tgtatactag cagatactat ccagtgaagc ataaattaga atttaatttg atgttcaaaa 2823

acagttccat ttttaagggt taaggtggta ttttcaagaa aaggcagaac aaataatgca 2883

aaattctcag taatagtgat acatggatat acttcctttt aaattctcag ctgcaaaata 2943

attgtagaca aaataatggc atttaactaa agatggagca tgatctaagt acatagcaca 3003

tgtgaataaa agaaaagctg acagtatatt ctggtttcaa taaaatgacc tatcagaaag 3063
```

```
tagaatttca tccccaagag tatttcagtt tatccaatat tgagtaagtt ctgaaacagt 3123

tttagaaaaa attttctttt tgttaaatgt gatgcactga tcaatttttg tcacagcatt 3183

ttcatacctt catggtggac tactagtcac tgcttccata aatattgttt acagggtgag 3243

atttggttta ttcatcttaa gtgctgtagc aaactgtggt tcgagcaacc tgtgggaaat 3303

ctgtgagagg gaatggggtg ggagatgtgg gggaatggtg gtcagactga tgacagatcc 3363

tagaccaatg taaagaatgt gtatctgtat ataaataatt tatcaaatag ttttctcttt 3423

gtgtctgtgt tagtgttttt aaagctgctc atttcatttt gtccaaccaa aaagaaaagg 3483

gagataacta atgagcttct agtgatgttc aaaattgctg ttaataggca ttataccctg 3543

caagttcact gcatgtctga tgcttggtaa aactagtctt ccctgtaaaa tgcagattac 3603

aggtattaaa gcaatctagt ggtatacccg ccccttgcct tagtaagagg agcagtgaaa 3663

tgtatatagt tgatgttcag tatttccaag taccattttt atatagtagc ttatttgacc 3723

ataagtcaca catcaaaaaa agattaccct tagtgtatgt gttttaatat tagaaaattg 3783

gcatatgtac tttatttttg aaaagggaag agatgggtgt ggggtggcaa tagcattgtg 3843

ccattttgtc atagaatgta aaaattggtt aactttacaa atgtcagcta gttttgacta 3903
```

```
ctaattgggg gaaatttttag ataatttttta aattcaaagt tatttataaa atgctagaat  3963

ttgttttaat tttttgtatt ttgagccact tcacatgaag actcagttgc atttttatcg  4023

aatacatttt tatcaacagt taaagactat ggtggttttt tcagagtttg gctaagaatg  4083

ttgttaccat cttctttgtt tgtggtacaa tattttcagt gcaaaagaga tgtcattcag  4143

ttaaaaagac aaacctctag atgtgtaatt acatggaaaa tactagcaat gtgaatgctt  4203

ttgtagtaac catcttgtag tacctgtgaa atctataact cagaaatggt cagatggtca  4263

ggagccagct atgcagcagt ataccatctg tttaattatt ttgtaggtcc tgtgtgtgga  4323

accaactata aacccagttc taaagttgtg tatgatggtg aaccttttggg aatagttctt  4383

atcaacttaa ttggatactt ttagcaaata ggaacttaat tctcagcact gaacatgaat  4443

tacttccttg gagttttttt tcattcatat ttttgttgtt tccaggaatt tatttgatat  4503

taatgggcgt aaaacagcat cattgtactt aagctatgga tgtttttatt ttatattttc  4563

tttatttata actgtgccaa gtattatttt gctacttacc gtgttattct gtggaaagaa  4623

aaacctgtaa agtgtttaat aaattagccc tccttacata aattaaatgt caaaattttg  4683

taaaatatta atcagaataa atactgactc tt                                  4715
```

<210> 67

<211> 498

<212> PRT

<213> Homo sapiens

<400> 67

```
Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
 1               5                  10                  15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
            20                  25                  30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
        35                  40                  45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
    50                  55                  60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
65                  70                  75                  80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
                85                  90                  95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
            100                 105                 110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
            115                 120                 125
```

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
　　130　　　　　　　　　135　　　　　　　　140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
　　145　　　　　　　　150　　　　　　　155　　　　　　　　160

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
　　　　　　　　165　　　　　　　　170　　　　　　　175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
　　　　　　180　　　　　　　　185　　　　　　　190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
　　　　195　　　　　　　　200　　　　　　　205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
　　210　　　　　　　　215　　　　　　　　220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Pro Gln Gln Phe Ile
225　　　　　　　　230　　　　　　　235　　　　　　　　240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
　　　　　　　245　　　　　　　250　　　　　　　255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
　　　　　260　　　　　　　　265　　　　　　　270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr

```
         275                    280                    285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
     290                    295                    300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305                    310                    315                    320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
                325                    330                    335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
                340                    345                    350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
                355                    360                    365

Met His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
     370                    375                    380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385                    390                    395                    400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
                405                    410                    415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
                420                    425                    430
```

```
Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
        435             440             445


Gly Gln Met Arg Pro Glu Gly Val Gly Leu Pro Ala Glu Val Thr Gln
        450             455             460


Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp
465             470             475             480


Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
        485             490             495


Ser Cys
```

<210> 68

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 68

```
gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct    51
                        Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                        1               5               10
```

```
cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac    99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
              15                  20                  25
```

```
gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att    147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile
              30                  35                  40
```

```
ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg    195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
              45                  50                  55
```

```
cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc    243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
          60                  65                  70
```

```
ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa    291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
      75                  80                  85                  90
```

```
gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct    339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
              95                  100                 105
```

```
gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg    387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
              110                 115                 120
```

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag   435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
         125   130   135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc   483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
         140   145   150

ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac   531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155   160   165   170

tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag   579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
                 175   180   185

gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg   627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
         190   195   200

acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg   675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
         205   210   215

cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct   723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
         220   225   230

ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg   771

```
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235             240             245             250


gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc    819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
            255             260             265


cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag    867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
            270             275             280


ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac    915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
            285             290             295


ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca    963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
            300             305             310


gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc   1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315             320             325             330


aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc   1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
            335             340             345


tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg   1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
```

```
                350                   355                   360

cac acc ctg aac agc acg atg cac gag tac aag atc caa ggc ctc tca   1155
His Thr Leu Asn Ser Thr Met His Glu Tyr Lys Ile Gln Gly Leu Ser
        365                   370                   375


tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc   1203
Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
        380                   385                   390


act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac   1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395                   400                   405                   410


ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc   1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
                      415                   420                   425


tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc   1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
                430                   435                   440


tcc agg tgg att gtt gag ggg cag atg aga cct gaa ggt gtt gga tta   1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg Pro Glu Gly Val Gly Leu
                445                   450                   455


cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca   1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
                460                   465                   470
```

```
aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc    1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475             480             485             490


cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat    1545
Gln Lys Leu Trp Glu Phe Ser Cys
                495


aaagaattca tatcatctgt taatggcgac agtttttgtt tcttcctttg aattttttat    1605


attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg    1665


gctaaagcgt cttctatcat atcgaattgg gacaatgata gaagacaatc tttgttttgt    1725


cactctaaag aaattattgt aagattttat catcaggtat gacatttaca ccattgatgt    1785


aggctttta aaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg    1845


atttcctagg agttggtttt tttttttta aagcataaat aaatttaatt gcatcag      1902
```

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<210> 69

<211> 498

<212> PRT

<213> Homo sapiens


<400> 69

Met Ala Arg Leu Glu Val Ile Glu Leu Pro His Ser Pro Gln Asn Leu
```

```
         1                5                    10                      15

Leu Val Ser Pro Asn Ser Ser His Ser His Ala Val Val Leu Ser Trp
             20                   25                   30

Val Arg Pro Phe Asp Gly Asn Ser Pro Ile Leu Tyr Tyr Ile Val Glu
             35                   40                   45

Leu Ser Glu Asn Asn Ser Pro Trp Lys Val His Leu Ser Asn Val Gly
             50                   55                   60

Pro Glu Met Thr Gly Val Thr Val Ser Gly Leu Thr Pro Ala Arg Thr
    65                   70                   75                   80

Tyr Gln Phe Arg Val Cys Ala Val Asn Glu Val Gly Arg Gly Gln Tyr
                 85                   90                   95

Ser Ala Glu Thr Ser Arg Leu Met Leu Pro Glu Glu Pro Pro Ser Ala
                 100                  105                  110

Pro Pro Lys Asn Ile Val Ala Ser Gly Arg Thr Asn Gln Ser Ile Met
                 115                  120                  125

Val Gln Trp Gln Pro Pro Pro Glu Thr Glu His Asn Gly Val Leu Arg
             130                  135                  140

Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly Leu Pro Gly Glu Tyr Gln
145                  150                  155                  160
```

出証特２００２－３０３２９３５

Gln Arg Asn Ile Thr Ser Pro Glu Val Asn Tyr Cys Leu Val Thr Asp
　　　　　　　　165　　　　　　　　　170　　　　　　　　175

Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln Val Ala Ala Tyr Asn Gly
　　　　　　　　180　　　　　　　　　185　　　　　　　　190

Ala Gly Leu Gly Val Phe Ser Arg Ala Val Thr Glu Tyr Thr Leu Gln
　　　　　　　　195　　　　　　　　　200　　　　　　　　205

Gly Val Pro Thr Ala Pro Pro Gln Asn Val Gln Thr Glu Ala Val Asn
　　210　　　　　　　　　215　　　　　　　　　220

Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro Pro Gln Gln Phe Ile
225　　　　　　　　　230　　　　　　　　235　　　　　　　　240

Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu Ala Trp Pro Ala Asp Ala
　　　　　　　　245　　　　　　　　　250　　　　　　　　255

Pro Glu Ala Val Thr Val Val Thr Ile Ala Pro Asp Phe His Gly Val
　　　　　　　　260　　　　　　　　　265　　　　　　　　270

His His Gly His Ile Thr Asn Leu Lys Lys Phe Thr Ala Tyr Phe Thr
　　　　　　　　275　　　　　　　　　280　　　　　　　　285

Ser Val Leu Cys Phe Thr Thr Pro Gly Asp Gly Pro Pro Ser Thr Pro
　　290　　　　　　　　　295　　　　　　　　　300

Gln Leu Val Trp Thr Gln Glu Asp Lys Pro Gly Ala Val Gly His Leu
305　　　　　　　　　310　　　　　　　　315　　　　　　　　320

Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu Lys Val Ser Trp Gln Glu
            325   330   335

Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly Tyr Gln Ile Ser Trp Glu
            340   345   350

Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr His Thr Leu Asn Ser Thr
            355   360   365

Thr His Glu Tyr Lys Ile Gln Gly Leu Ser Ser Leu Thr Thr Tyr Thr
            370   375   380

Ile Asp Val Ala Ala Val Thr Ala Val Gly Thr Gly Leu Val Thr Ser
385   390   395   400

Ser Thr Ile Ser Ser Gly Val Pro Pro Asp Leu Pro Gly Ala Pro Ser
            405   410   415

Asn Leu Val Ile Ser Asn Ile Ser Pro Arg Ser Ala Thr Leu Gln Phe
            420   425   430

Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile Ser Arg Trp Ile Val Glu
            435   440   445

Gly Gln Met Arg His Gln Gly Val Gly Leu Pro Ala Glu Val Thr Gln
            450   455   460

Pro Ser His Glu Ala Gly Leu Glu Pro Ala Asn Leu Gly Ser Leu Trp

465   470   475   480

Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser Gln Lys Leu Trp Glu Phe
                     485   490   495

Ser Cys

<210> 70

<211> 1902

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (22)..(1515)

<400> 70

gaaggaggga atgactccag g atg gcc cgg ctg gaa gtg att gaa ctg cct   51
                        Met Ala Arg Leu Glu Val Ile Glu Leu Pro
                        1   5   10

cat tca cct cag aac ctc ctg gtc agc cct aat tct tcc cac agc cac   99
His Ser Pro Gln Asn Leu Leu Val Ser Pro Asn Ser Ser His Ser His
            15   20   25

gcc gtg gtg ctc tct tgg gtc cgg ccc ttt gat gga aac agt cct att   147
Ala Val Val Leu Ser Trp Val Arg Pro Phe Asp Gly Asn Ser Pro Ile

```
               30                      35                      40

ctt tat tac atc gtg gag ctg tct gaa aac aac tct cca tgg aag gtg    195
Leu Tyr Tyr Ile Val Glu Leu Ser Glu Asn Asn Ser Pro Trp Lys Val
         45                      50                      55

cat ctg tca aac gtt ggc cct gag atg aca ggc gtc acc gtg agt ggc    243
His Leu Ser Asn Val Gly Pro Glu Met Thr Gly Val Thr Val Ser Gly
     60                      65                      70

ctg act ccg gct cgt acc tat caa ttc cgg gtg tgc gcg gtg aat gaa    291
Leu Thr Pro Ala Arg Thr Tyr Gln Phe Arg Val Cys Ala Val Asn Glu
 75                      80                      85                      90

gtg ggc agg ggc cag tac agt gcc gag aca agc agg ttg atg cta cct    339
Val Gly Arg Gly Gln Tyr Ser Ala Glu Thr Ser Arg Leu Met Leu Pro
                     95                     100                     105

gaa gaa cca ccc agt gct ccc ccg aaa aat ata gtg gcc agt ggg cgg    387
Glu Glu Pro Pro Ser Ala Pro Pro Lys Asn Ile Val Ala Ser Gly Arg
                110                     115                     120

act aat cag tcc att atg gtc cag tgg cag cca ccc cca gaa aca gag    435
Thr Asn Gln Ser Ile Met Val Gln Trp Gln Pro Pro Pro Glu Thr Glu
                125                     130                     135

cac aac ggg gtg ttg cgt gga tac atc ctc agg tac cgc ctg gct ggc    483
His Asn Gly Val Leu Arg Gly Tyr Ile Leu Arg Tyr Arg Leu Ala Gly
            140                     145                     150
```

```
ctt ccc gga gag tac cag cag cgg aac atc acc agc ccg gag gtg aac    531
Leu Pro Gly Glu Tyr Gln Gln Arg Asn Ile Thr Ser Pro Glu Val Asn
155             160             165             170


tac tgc ctg gtg aca gac ctg atc atc tgg aca cag tat gag ata cag    579
Tyr Cys Leu Val Thr Asp Leu Ile Ile Trp Thr Gln Tyr Glu Ile Gln
                175             180             185


gtg gcg gcg tac aac ggg gcc ggt ctg ggc gtc ttc agc agg gca gtg    627
Val Ala Ala Tyr Asn Gly Ala Gly Leu Gly Val Phe Ser Arg Ala Val
                190             195             200


acc gag tac acc ttg cag gga gtg ccc acc gcg ccc ccg cag aac gtg    675
Thr Glu Tyr Thr Leu Gln Gly Val Pro Thr Ala Pro Pro Gln Asn Val
                205             210             215


cag acg gaa gcc gtg aac tcc acc acc att cag ttc ctg tgg aac cct    723
Gln Thr Glu Ala Val Asn Ser Thr Thr Ile Gln Phe Leu Trp Asn Pro
            220             225             230


ccg cct cag cag ttt atc aat ggc atc aac cag gga tac aag ctt ctg    771
Pro Pro Gln Gln Phe Ile Asn Gly Ile Asn Gln Gly Tyr Lys Leu Leu
235             240             245             250


gca tgg ccg gca gat gcc ccc gag gct gtc act gtg gtc act att gcc    819
Ala Trp Pro Ala Asp Ala Pro Glu Ala Val Thr Val Val Thr Ile Ala
                255             260             265
```

cca gat ttc cac gga gtc cac cat gga cac ata acg aac ctg aag aag   867
Pro Asp Phe His Gly Val His His Gly His Ile Thr Asn Leu Lys Lys
           270   275   280

ttt acc gcc tac ttc act tcc gtt ctg tgc ttc acc acc cct ggg gac   915
Phe Thr Ala Tyr Phe Thr Ser Val Leu Cys Phe Thr Thr Pro Gly Asp
           285   290   295

ggg cct ccc agc aca cct cag ctg gtc tgg act cag gaa gac aaa cca   963
Gly Pro Pro Ser Thr Pro Gln Leu Val Trp Thr Gln Glu Asp Lys Pro
           300   305   310

gga gct gtg gga cat ctg agt ttc aca gag atc ttg gac aca tct ctc   1011
Gly Ala Val Gly His Leu Ser Phe Thr Glu Ile Leu Asp Thr Ser Leu
315   320   325   330

aag gtc agc tgg cag gag ccc ctg gag aaa aat ggc atc att act ggc   1059
Lys Val Ser Trp Gln Glu Pro Leu Glu Lys Asn Gly Ile Ile Thr Gly
                335   340   345

tat cag atc tct tgg gaa gtg tac ggc agg aac gac tct cgt ctc acg   1107
Tyr Gln Ile Ser Trp Glu Val Tyr Gly Arg Asn Asp Ser Arg Leu Thr
                350   355   360

cac acc ctg aac agc acg acg cac gag tac aag atc caa ggc ctc tca   1155
His Thr Leu Asn Ser Thr Thr His Glu Tyr Lys Ile Gln Gly Leu Ser
           365   370   375

tct ctc acc acc tac acc atc gac gtg gcc gct gtg act gcc gtg ggc   1203

Ser Leu Thr Thr Tyr Thr Ile Asp Val Ala Ala Val Thr Ala Val Gly
    380   385   390

act ggc ctg gtg act tca tcc acc att tct tct gga gtg ccc cca gac   1251
Thr Gly Leu Val Thr Ser Ser Thr Ile Ser Ser Gly Val Pro Pro Asp
395   400   405   410

ctt cct ggt gcc cca tcc aac ctg gtc att tcc aac atc agc cct cgc   1299
Leu Pro Gly Ala Pro Ser Asn Leu Val Ile Ser Asn Ile Ser Pro Arg
                 415   420   425

tcc gcc acc ctt cag ttc cgg cca ggc tat gac ggg aaa acg tcc atc   1347
Ser Ala Thr Leu Gln Phe Arg Pro Gly Tyr Asp Gly Lys Thr Ser Ile
             430   435   440

tcc agg tgg att gtt gag ggg cag atg aga cat caa ggt gtt gga tta   1395
Ser Arg Trp Ile Val Glu Gly Gln Met Arg His Gln Gly Val Gly Leu
             445   450   455

cct gcc gag gtc aca cag cca agc cat gaa gcc gga ttg gag cct gca   1443
Pro Ala Glu Val Thr Gln Pro Ser His Glu Ala Gly Leu Glu Pro Ala
             460   465   470

aac ctc gga agt ctg tgg ctg ctc agc ctg gtg tat tgg tgt tac agc   1491
Asn Leu Gly Ser Leu Trp Leu Leu Ser Leu Val Tyr Trp Cys Tyr Ser
475   480   485   490

cag aaa ctt tgg gaa ttc tct tgt tagttggtta gttttactgt aattttctat   1545
Gln Lys Leu Trp Glu Phe Ser Cys

495

aaagaattca tatcatctgt taatggcgac agttttttgtt cttcctttg aattttttat 1605

attctttctt tctctttttt gtttcttctt ctttgagtat tttgtaatct tactgggagg 1665

gctaaagcgt cttctatcat atcgaattgg dacaatgata gaagacaatc tttgtttttgt 1725

cactctaaag aaattattgt aagattttat catcaggtat dacatttaca ccattgatgt 1785

aggctttttta aaaaatatat ccagcctgta ttgggttaag atgattcttt tctgatcctg 1845

atttcctagg agttggtttt ttttttttta aagcataaat aaatttaatt gcatcag 1902

<210> 71

<211> 245

<212> PRT

<213> Homo sapiens

<400> 71

Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser Met His
1   5   10   15

Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser Met Thr
                20   25   30

Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile Leu Thr
                35   40   45

```
Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His Arg Pro
    50              55              60

Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly
    65          70              75                  80

Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro
                85              90              95

Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp
            100             105             110

Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr
        115             120             125

Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala
    130             135             140

Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu
145             150             155             160

Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys
                165             170             175

Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly
            180             185             190

Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val
```

```
            195                 200                 205
```

Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile Val Arg
```
            210                 215                 220
```

Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val Leu Gly
```
    225                 230                 235                 240
```

Gln Trp Ile Gln Arg
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                        245
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<210> 72

<211> 1551

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (127)..(861)

<400> 72

ggaagtcggc caccttcctc cgtcccggcc gttagcccag ccaagcccag ccaagcccag 60

ccaagccccg ccgatcgcgg gcaccggagc cagccccgca gcgggtcccg cctgtctgtc 120

acgctg atg ccc gtg cag ctg tct gag cac ccg gaa tgg aat gag tct   168
        Met Pro Val Gln Leu Ser Glu His Pro Glu Trp Asn Glu Ser
        1   5   10

atg cac tcc ctc cgg atc agt gtg ggg ggc ctt cct gtg ctg gcg tcc   216
Met His Ser Leu Arg Ile Ser Val Gly Gly Leu Pro Val Leu Ala Ser
15   20   25   30

atg acc aag gcc gcg gac ccc cgc ttc cgc ccc cgc tgg aag gtg atc   264
Met Thr Lys Ala Ala Asp Pro Arg Phe Arg Pro Arg Trp Lys Val Ile
          35   40   45

ctg acg ttc ttt gtg ggt gct gcc atc ctc tgg ctg ctc tgc tcc cac   312
Leu Thr Phe Phe Val Gly Ala Ala Ile Leu Trp Leu Leu Cys Ser His
          50   55   60

cgc ccg gcc ccc ggc agg ccc ccc acc cac aat gca cac aac tgg agg   360
Arg Pro Ala Pro Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg
          65   70   75

ctc ggc cag gcg ccc gcc aac tgg tac aat gac acc tac ccc ctg tct   408
Leu Gly Gln Ala Pro Ala Asn Trp Tyr Asn Asp Thr Tyr Pro Leu Ser
       80   85   90

ccc cca caa agg aca ccg gct ggg att cgg tat cga atc gca gtt atc   456
Pro Pro Gln Arg Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile
95   100   105   110

gca gac ctg gac aca gag tca agg gcc caa gag gaa aac acc tgg ttc   504
Ala Asp Leu Asp Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe
          115   120   125

```
agt tac ctg aaa aag ggc tac ctg acc ctg tca gac agt ggg gac aag    552
Ser Tyr Leu Lys Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys
            130               135               140

gtg gcc gtg gaa tgg gac aaa gac cat ggg gtc ctg gag tcc cac ctg    600
Val Ala Val Glu Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu
            145               150               155

gcg gag aag ggg aga ggc atg gag cta tcc gac ctg att gtt ttc aat    648
Ala Glu Lys Gly Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn
            160               165               170

ggg aaa ctc tac tcc gtg gat gac cgg acg ggg gtc gtc tac cag atc    696
Gly Lys Leu Tyr Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile
175               180               185               190

gaa ggc agc aaa gcc gtg ccc tgg gtg att ctg tcc gac ggc gac ggc    744
Glu Gly Ser Lys Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly
            195               200               205

acc gtg gag aaa ggc ttc aag gcc gaa tgg ctg gca gtg cgg gag att    792
Thr Val Glu Lys Gly Phe Lys Ala Glu Trp Leu Ala Val Arg Glu Ile
            210               215               220

gta agg aag cgg tgg cgg ctg gtg aag caa gtc tca cat gtc ggc gtt    840
Val Arg Lys Arg Trp Arg Leu Val Lys Gln Val Ser His Val Gly Val
            225               230               235

ctt ggc caa tgg ata caa aga taaagaaaat gttgcctttt tctaggaact       891
Leu Gly Gln Trp Ile Gln Arg
```

Leu Gly Gln Trp Ile Gln Arg
　　　 240　　　　　　 245

gtcagaaatc ctcatgcctt tcaagacttc tgtgaatgac ttgaattttt tattccctgc 951

ctagggtctg tgaacgaggc ctgtctcttc cctgggggttt ctttccatgg cctttatttc 1011

tcctcttcca gtgggagttt tgcaggctct tctctgtgga aacttcacga gcgttggctg 1071

ggcctcggct tcgctggagt gtactccagg gtgaaggcag agtgggattt gagacccagg 1131

tagtggagga agcgaaggaa gtgaacgctg aatgtgacgc atttctgaag agctcagctg 1191

tcaccgggca tagcctggaa gccccaagtc tgttctgact ttgcctggct gtctccttga 1251

cccgcctcct agatcattgt ccttgatgtc caggctgggt catttaaaat agagatgcaa 1311

tcaggaaggt tgggggactt gggactgtgg ctgaattgag accttgctga tgtattcatg 1371

tcagcacctg agtcacagcc caggtgcccg gaagcagcct cttcgcatag gcagtgattt 1431

gcgattactt taaagctcac ctttttctt ccctctctg ttcgctgctg tcagcataat 1491

gattgtgttc cttccctatg ggatccatct gttttgtaaa caataaagcg tctgagggag 1551

<210> 73

<211> 352

<212> PRT

<213> Homo sapiens

<400> 73

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
1   5   10   15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
                20   25   30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
            35   40   45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
        50   55   60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
65   70   75   80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
                85   90   95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
            100   105   110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
            115   120   125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
            130   135   140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145   150   155   160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
                165   170   175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
                180   185   190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
                195   200   205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
                210   215   220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225   230   235   240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
                245   250   255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
                260   265   270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
                275   280   285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val

```
        290                 295                 300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305                 310                 315                 320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
                325                 330                 335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
                340                 345                 350
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<210> 74

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 74

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ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc   60

tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga      114
                                              Met Glu Ser Gly
                                               1

ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
```

Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
5   10   15   20

gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                    25   30   35

caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag   258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                    40   45   50

agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata   306
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
               55   60   65

gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg   354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
     70   75   80

gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag   402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
85   90   95   100

atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc   450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
               105   110   115

att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag   498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu

```
                120                     125                       130


gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg    546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
        135                    140                     145


gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag    594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
        150                    155                     160


tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa    642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
165                    170                     175                   180


ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca    690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
                185                    190                     195


ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg    738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
                200                    205                     210


ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc    786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
                215                    220                     225


ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg    834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
        230                    235                     240
```

```
ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg     882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245             250             255             260


aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag     930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
            265             270             275


gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct     978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
            280             285             290


gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc    1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
            295             300             305


ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc    1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
            310             315             320


gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga    1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325             330             335             340


cag gcg atc acc cgg gtg ata ccc ccg tac aac agc taatagtttg         1168
Gln Ala Ile Thr Arg Val Ile Pro Pro Tyr Asn Ser
            345             350
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gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228

ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288

tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348

gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408

tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468

caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggtgaatcg 1528

ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt cttttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068
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tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagccttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctctttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc   2401

<210> 75

<211> 352

<212> PRT

<213> Homo sapiens

<400> 75

Met Glu Ser Gly Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly
1   5   10   15

Thr Thr Ser Val Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys
                20   25   30

Ala Arg Val Ser Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly
            35   40   45

Glu Asp Leu Lys Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro
     50   55   60

Tyr Ala Val Ile Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn
     65   70   75   80

Ser Gln Phe Val Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu
          85   90   95

Gln Glu His Lys Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp
        100   105   110

Cys Ser Lys Ile Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu
        115   120   125

Val Pro His Glu Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro
        130   135   140

Leu Asp Ser Val Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His
145   150   155   160

Pro Ser Ile Gln Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly
        165   170   175

Glu Arg Pro Lys Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly
        180   185   190

Ala Thr Leu Thr Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val
        195   200   205

Arg Leu Gln Pro Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln
    210   215   220

Asp Phe Asp Ser Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp
225   230   235   240

Lys Val Leu Ala Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe
                    245   250   255

Phe Ile Leu Arg Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu
                260   265   270

Lys Gln Met Gln Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser
            275   280   285

Arg Ala Lys Pro Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val
    290   295   300

Cys Leu Ser Ser Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val
305   310   315   320

Cys Ser Cys Thr Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys
                325   330   335

Pro Ile Cys Arg Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
                340   345   350

<210> 76

<211> 2401

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103)..(1158)

<400> 76

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ttaggccggg ggggtgcggt cctggtcgga aggaggtgga gagtcggggg tcaccaggcc   60


tatccttggc gccacagtcg gccaccgggg ctcgccgccg tc atg gag agc gga      114
                                               Met Glu Ser Gly
                                                 1


ggg cgg ccc tcg ctg tgc cag ttc atc ctc ctg ggc acc acc tct gtg   162
Gly Arg Pro Ser Leu Cys Gln Phe Ile Leu Leu Gly Thr Thr Ser Val
  5                  10                  15                  20


gtc acc gcc gcc ctg tac tcc gtg tac cgg cag aag gcc cgg gtc tcc   210
Val Thr Ala Ala Leu Tyr Ser Val Tyr Arg Gln Lys Ala Arg Val Ser
                    25                  30                  35


caa gag ctc aag gga gct aaa aaa gtt cat ttg ggt gaa gat tta aag   258
Gln Glu Leu Lys Gly Ala Lys Lys Val His Leu Gly Glu Asp Leu Lys
                40                  45                  50


agt att ctt tca gaa gct cca gga aaa tgc gtg cct tat gct gtt ata   306
```

```
Ser Ile Leu Ser Glu Ala Pro Gly Lys Cys Val Pro Tyr Ala Val Ile
            55                  60                  65


gaa gga gct gtg cgg tct gtt aaa gaa acg ctt aac agc cag ttt gtg    354
Glu Gly Ala Val Arg Ser Val Lys Glu Thr Leu Asn Ser Gln Phe Val
            70                  75                  80


gaa aac tgc aag ggg gta att cag cgg ctg aca ctt cag gag cac aag    402
Glu Asn Cys Lys Gly Val Ile Gln Arg Leu Thr Leu Gln Glu His Lys
            85                  90                  95              100


atg gtg tgg aat cga acc acc cac ctt tgg aat gat tgc tca aag atc    450
Met Val Trp Asn Arg Thr Thr His Leu Trp Asn Asp Cys Ser Lys Ile
                    105                 110                 115


att cat cag agg acc aac aca gtg ccc ttt gac ctg gtg ccc cac gag    498
Ile His Gln Arg Thr Asn Thr Val Pro Phe Asp Leu Val Pro His Glu
                    120                 125                 130


gat ggc gtg gat gtg gct gtg cga gtg ctg aag ccc ctg gac tca gtg    546
Asp Gly Val Asp Val Ala Val Arg Val Leu Lys Pro Leu Asp Ser Val
            135                 140                 145


gat ctg ggt cta gag act gtg tat gag aag ttc cac ccc tcg att cag    594
Asp Leu Gly Leu Glu Thr Val Tyr Glu Lys Phe His Pro Ser Ile Gln
            150                 155                 160


tcc ttc acc gat gtc atc ggc cac tac atc agc ggt gag cgg ccc aaa    642
Ser Phe Thr Asp Val Ile Gly His Tyr Ile Ser Gly Glu Arg Pro Lys
```

```
         165                  170                  175                  180

ggc atc caa gag acc gag gag atg ctg aag gtg ggg gcc acc ctc aca     690
Gly Ile Gln Glu Thr Glu Glu Met Leu Lys Val Gly Ala Thr Leu Thr
                  185                  190                  195


ggg gtt ggc gaa ctg gtc ctg gac aac aac tct gtc cgc ctg cag ccg     738
Gly Val Gly Glu Leu Val Leu Asp Asn Asn Ser Val Arg Leu Gln Pro
                  200                  205                  210


ccc aaa caa ggc atg cag tac tat cta agc agc cag gac ttc gac agc     786
Pro Lys Gln Gly Met Gln Tyr Tyr Leu Ser Ser Gln Asp Phe Asp Ser
              215                  220                  225


ctg ctg cag agg cag gag tcg agc gtc agg ctc tgg aag gtg ctg gcg     834
Leu Leu Gln Arg Gln Glu Ser Ser Val Arg Leu Trp Lys Val Leu Ala
      230                  235                  240


ctg gtt ttt ggc ttt gcc aca tgt gcc acc ctc ttc ttc att ctc cgg     882
Leu Val Phe Gly Phe Ala Thr Cys Ala Thr Leu Phe Phe Ile Leu Arg
245                  250                  255                  260


aag cag tat ctg cag cgg cag gag cgc ctg cgc ctc aag cag atg cag     930
Lys Gln Tyr Leu Gln Arg Gln Glu Arg Leu Arg Leu Lys Gln Met Gln
                  265                  270                  275


gag gag ttc cag gag cat gag gcc cag ctg ctg agc cga gcc aag cct     978
Glu Glu Phe Gln Glu His Glu Ala Gln Leu Leu Ser Arg Ala Lys Pro
                  280                  285                  290
```

```
gag gac agg gag agt ctg aag agc gcc tgt gta gtg tgt ctg agc agc    1026
Glu Asp Arg Glu Ser Leu Lys Ser Ala Cys Val Val Cys Leu Ser Ser
        295             300             305


ttc aag tcc tgc gtc ttt ctg gag tgt ggg cac gtt tgt tcc tgc acc    1074
Phe Lys Ser Cys Val Phe Leu Glu Cys Gly His Val Cys Ser Cys Thr
        310             315             320


gag tgc tac cgc gcc ttg cca gag ccc aag aag tgc cct atc tgc aga    1122
Glu Cys Tyr Arg Ala Leu Pro Glu Pro Lys Lys Cys Pro Ile Cys Arg
325             330             335             340


cag gcg atc acc cgg gtg ata ccc ctg tac aac agc taatagtttg         1168
Gln Ala Ile Thr Arg Val Ile Pro Leu Tyr Asn Ser
            345             350


gaagccgcac agcttgacct ggaagcaccc ctgccccctt ttcagggatt tttatctcga 1228


ggcctttgga ggagcagtgg tgggggtagc tgtcacctcc aggtatgatt gagggaggaa 1288


tcgggtagaa actctccaga cccatgcctc caatggcagg atgctgcctt tcccacctga 1348


gaggggaccc tgtccatgtg cagcctcatc agagcctcac cctgggagga tgccgtggcg 1408


tctcctccca ggagccagat cagtgcgagt gtgactgaaa atgcctcatc acttaagcac 1468


caaagccagt gatcagcagc tcttctgttc ctgtgtcttc tgtttttttc tggtgaatcg 1528
```

```
ttgcttgctg tggacttggt ggaggactca gaggggagga aaggctgggc cccgagtaca 1588

acggatgcct tgggtgctgc ctccgaagag actctgccgc agcttttctt ctttttcctc 1648

atgccccggg aaacagtctt tcttcagaat tgtcaggctg ggcaggtcaa cttgtgttcc 1708

tttcccctca cctgcttgcc tccttaacgc ctgcacgtgt gtgtagagga caaaagaaag 1768

tgaagtcagc acatccgctt ctgcccagat ggtcggggcc ccgggcaaca gattgaagag 1828

agatcatgtg aagggcagtt ggtcaggcag gcctcctggt ttcgccactg gccctgattt 1888

gaactcctgc cacttgggag agctcggggt ggtccctggt tttccctcct ggagaatgag 1948

gcgcagaggc ctcgcctcct gaaggacgca gtgtggatgc cactggccta gtgtcctggc 2008

ctcacagctt ccttgcaagg ctgtcacaag gaaaagcagc cggctggcac cctgagcata 2068

tgccctcttg gggctccctc atccagcccg tcgcagcttt gacatcttgg tgtactcatg 2128

tcgcttctcc ttgtgttacc ccctcccagt attaccattt gcccctcacc tgcccttggt 2188

gagcctttta gtgcaagaca gatggggctg ttttccccca cctctgagta gttggaggtc 2248

acatacacag ctcttttttt attgcccttt tctgcctctg aatgttcatc tctcgtcctc 2308

ctttgtgcag gcgaggaagg ggtgccctca ggggccgaca ctagtgtgat gcagtgtcca 2368

gtgtgaacag cagaaattaa acatgttgca acc                          2401
```

<210> 77

<211> 697

<212> PRT

<213> Homo sapiens

<400> 77

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Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu Tyr Leu Ala
1               5                   10                  15

Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met His Ser Ser
                20                  25                  30

Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu Val Ala Ile
            35                  40                  45

Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn Ser Leu Ile
        50                  55                  60

Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile Ala Ser Ile
65                  70                  75                  80

Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser Leu Ser Asn
                85                  90                  95

Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser
                100                 105                 110
```

Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu
        115   120   125

Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg Ile Ser
        130   135   140

Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu Phe Leu
        145   150   155   160

Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val Glu Lys
               165   170   175

Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu Ile Ile
             180   185   190

Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val Ile Phe
             195   200   205

Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile
             210   215   220

Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp
225   230   235   240

Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro Phe Leu
               245   250   255

Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala Gly Met
             260   265   270

Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr
275   280   285

His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe
290   295   300

Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly Phe His
305   310   315   320

Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg Thr Asp
                 325   330   335

Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg His Phe
                 340   345   350

Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala Thr Ala
     355   360   365

Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser
     370   375   380

Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe
385   390   395   400

His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile
                 405   410   415

Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu

```
                420                      425                      430

Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu
         435                 440                 445

Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly
         450                 455                 460

Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His Ser Lys
465                 470                 475                 480

Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg His Asp
                485                 490                 495

Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly Glu Trp
                500                 505                 510

Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp
         515                 520                 525

Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile Val Leu
         530                 535                 540

Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys Ile Asn
545                 550                 555                 560

Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr Val Asp
                565                 570                 575
```

Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp
    580   585   590

Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys
    595   600   605

Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp Ser Asp
    610   615   620

Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His Trp Met
625   630   635   640

Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala Asn Trp
      645   650   655

Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys
    660   665   670

Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu Asp Thr
    675   680   685

Gly Gln Gly Phe Lys Leu Val Lys Ser
    690   695

<210> 78

<211> 3008

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (372)..(2462)

<400> 78

cgtaccgtcg cggatttcgg cggcggaaac atggcggtcg cggccgggcc ggtaacggag 60

aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aattttttgta acgtgaggga aaagcccaca 360

```
ttgctggtta c atg tgt aaa tca ctg cgt tat tgc ttt agt cat tgt ctc   410
              Met Cys Lys Ser Leu Arg Tyr Cys Phe Ser His Cys Leu
               1               5                  10
```

```
tat tta gca atg aca aga ctg gaa gaa gta aat aga gaa gtg aac atg   458
Tyr Leu Ala Met Thr Arg Leu Glu Glu Val Asn Arg Glu Val Asn Met
     15              20                  25
```

```
cat tct tca gtg cgg tat ctt ggc tat tta gcc aga atc aat tta ttg   506
His Ser Ser Val Arg Tyr Leu Gly Tyr Leu Ala Arg Ile Asn Leu Leu
30              35                  40                  45
```

```
gtt gct ata tgc tta ggt cta tac gta aga tgg gaa aaa aca gca aat        554
Val Ala Ile Cys Leu Gly Leu Tyr Val Arg Trp Glu Lys Thr Ala Asn
            50                  55                  60


tcc tta att ttg gta att ttt att ctt ggt ctt ttt gtt ctt gga atc        602
Ser Leu Ile Leu Val Ile Phe Ile Leu Gly Leu Phe Val Leu Gly Ile
                65                  70                  75


gcc agc ata ctc tat tac tat ttt tca atg gaa gca gca agt tta agt        650
Ala Ser Ile Leu Tyr Tyr Tyr Phe Ser Met Glu Ala Ala Ser Leu Ser
            80                  85                  90


ctc tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt        698
Leu Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu
        95                  100                 105


gat aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat        746
Asp Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr
110                 115                 120                 125


ttg ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag        794
Leu Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu
                130                 135                 140


aga att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt        842
Arg Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val
                145                 150                 155
```

gaa ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg   890
Glu Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu
           160   165   170

gtg gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg   938
Val Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met
  175   180   185

ctg att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta   986
Leu Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu
190   195   200   205

gtt att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa   1034
Val Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys
           210   215   220

aat ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct   1082
Asn Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro
           225   230   235

ttc ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa   1130
Phe Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys
           240   245   250

ccc ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt   1178
Pro Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe
        255   260   265

gct gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt   1226

```
Ala Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu
270             275             280             285


aga gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt   1274
Arg Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe
                290             295             300


gga att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg   1322
Gly Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp
            305             310             315


gga ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac   1370
Gly Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His
            320             325             330


agg aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg   1418
Arg Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met
        335             340             345


cgc cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt   1466
Arg His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu
350             355             360             365


gca aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att   1514
Ala Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile
                370             375             380


ttc ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat   1562
Phe Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His
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                385                 390                 395

ggg ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga    1610
Gly Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly
        400                 405                 410


tat gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca    1658
Tyr Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro
        415                 420                 425


aca ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act    1706
Thr Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr
430                 435                 440                 445


ggc atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag    1754
Gly Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu
                450                 455                 460


acc tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg    1802
Thr Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu
        465                 470                 475


cat tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc    1850
His Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro
        480                 485                 490


aga cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca    1898
Arg His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr
        495                 500                 505
```

　　　　出証特２００２－３０３２９３５

```
gga gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt   1946
Gly Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu
510             515             520             525


ata gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att   1994
Ile Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile
                530             535             540


atc gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg   2042
Ile Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg
                545             550             555


aaa att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa   2090
Lys Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys
        560             565             570


aca gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca   2138
Thr Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr
    575             580             585


aaa gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg   2186
Lys Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp
590             595             600             605


act gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg   2234
Thr Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg
            610             615             620
```

tgg agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag   2282
Trp Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys
             625   630   635

cac tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg   2330
His Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu
             640   645   650

gca aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt   2378
Ala Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys
             655   660   665

ttt agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg   2426
Phe Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val
670   675   680   685

ctg gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac   2472
Leu Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
             690   695

cccaaagcgg gatattaata agcactcata ctaccaatta tcactaactt gccatttttt 2532

gtatgctgta tttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg 2592

tcttttctta agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa 2652

gtatgtaggg agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca 2712

ctttcaggaa tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa 2772

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tggtcaatga tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat 2832

gtagaccaga taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt 2892

ctttttcca  aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct 2952

tagaaaagaa agagggcagc ctaaataaa  cgcaaaattt gcttatactc catcac       3008
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<210> 79

<211> 611

<212> PRT

<213> Homo sapiens

<400> 79

Met Glu Ala Ala Ser Leu Ser Leu Ser Asn Leu Trp Phe Gly Phe Leu
1   5   10   15

Leu Gly Leu Leu Cys Phe Leu Asp Asn Ser Ser Phe Lys Asn Asp Val
            20   25   30

Lys Glu Glu Ser Thr Lys Tyr Leu Leu Leu Thr Ser Ile Val Leu Arg
            35   40   45

Ile Leu Cys Ser Leu Val Glu Arg Ile Ser Gly Tyr Val Arg His Arg
        50   55   60

Pro Thr Leu Leu Thr Thr Val Glu Phe Leu Glu Leu Val Gly Phe Ala

```
        65                      70                      75                      80

Ile Ala Ser Thr Thr Met Leu Val Glu Lys Ser Leu Ser Val Ile Leu
                    85                      90                      95

Leu Val Val Ala Leu Ala Met Leu Ile Ile Asp Leu Arg Met Lys Ser
                    100                     105                     110

Phe Leu Ala Ile Pro Asn Leu Val Ile Phe Ala Val Leu Leu Phe Phe
                    115                     120                     125

Ser Ser Leu Glu Thr Pro Lys Asn Pro Ile Ala Phe Ala Cys Phe Phe
        130                     135                     140

Ile Cys Leu Ile Thr Asp Pro Phe Leu Asp Ile Tyr Phe Ser Gly Leu
145                     150                     155                     160

Ser Val Thr Glu Arg Trp Lys Pro Phe Leu Tyr Arg Gly Arg Ile Cys
                    165                     170                     175

Arg Arg Leu Ser Val Val Phe Ala Gly Met Ile Glu Leu Thr Phe Phe
                    180                     185                     190

Ile Leu Ser Ala Phe Lys Leu Arg Asp Thr His Leu Trp Tyr Phe Val
                    195                     200                     205

Ile Pro Gly Phe Ser Ile Phe Gly Ile Phe Trp Met Ile Cys His Ile
                    210                     215                     220
```

Ile Phe Leu Leu Thr Leu Trp Gly Phe His Thr Lys Leu Asn Asp Cys
225   230   235   240

His Lys Val Tyr Phe Thr His Arg Thr Asp Tyr Asn Ser Leu Asp Arg
            245   250   255

Ile Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile Ser Glu Gln
            260   265   270

Leu Val Phe Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly Ala Val Ser
            275   280   285

Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu Ile Val Leu
            290   295   300

Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu Gly Asn Cys
305   310   315   320

Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro Thr Asn Phe
            325   330   335

Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu His Val Gln
            340   345   350

Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile Gln Arg Phe
            355   360   365

Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr Ser Thr Ser
            370   375   380

Gly Leu Ser Phe Asp Thr Leu His Ser Lys Leu Lys Ala Phe Leu Glu
385   390   395   400

Leu Arg Thr Val Asp Gly Pro Arg His Asp Thr Tyr Ile Leu Tyr Tyr
            405   410   415

Ser Gly His Thr His Gly Thr Gly Glu Trp Ala Leu Ala Gly Gly Asp
            420   425   430

Thr Leu Arg Leu Asp Thr Leu Ile Glu Trp Trp Arg Glu Lys Asn Gly
        435   440   445

Ser Phe Cys Ser Arg Leu Ile Ile Val Leu Asp Ser Glu Asn Ser Thr
        450   455   460

Pro Trp Val Lys Glu Val Arg Lys Ile Asn Asp Gln Tyr Ile Ala Val
465   470   475   480

Gln Gly Ala Glu Leu Ile Lys Thr Val Asp Ile Glu Glu Ala Asp Pro
            485   490   495

Pro Gln Leu Gly Asp Phe Thr Lys Asp Trp Val Glu Tyr Asn Cys Asn
            500   505   510

Ser Ser Asn Asn Ile Cys Trp Thr Glu Lys Gly Arg Thr Val Lys Ala
            515   520   525

Val Tyr Gly Val Ser Lys Arg Trp Ser Asp Tyr Thr Leu His Leu Pro

```
          530                    535                    540
```

Thr Gly Ser Asp Val Ala Lys His Trp Met Leu His Phe Pro Arg Ile

```
545                    550                    555                    560
```

Thr Tyr Pro Leu Val His Leu Ala Asn Trp Leu Cys Gly Leu Asn Leu

```
                   565                    570                    575
```

Phe Trp Ile Cys Lys Thr Cys Phe Arg Cys Leu Lys Arg Leu Lys Met

```
                   580                    585                    590
```

Ser Trp Phe Leu Pro Thr Val Leu Asp Thr Gly Gln Gly Phe Lys Leu

```
                   595                    600                    605
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Val Lys Ser

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          610
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<210> 80

<211> 3007

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (629)..(2461)

<400> 80

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aaagtttacg ccgacactgg cctgtattag cgcgtatggc ctcgggccct cgttccccaa 120

ggcgtgccgc ctccctgttc tcagtcgcag gctgaagcct tgtctgctct cctccttttt 180

ggtttggttt tggaactgac tccgagggtt gggagagcgc gttggtggcg acggccgagt 240

cagatcacta taaacaaaat ttccacaaga gaaaatgttg aaataggagt tgcggataca 300

ttggatatac tggatgaaat acaagcggtt aatttttgta acgtgaggga aaagcccaca 360

ttgctggtta catgtgtaaa tcactgcgtt attgctttag tcattgtctc tatttagcaa 420

tgacaagact ggaagaagta aatagagaag tgaacatgca ttcttcagtg cggtatcttg 480

ctatttagcc agaatcaatt tattggttgc tatatgctta ggtctatacg taagatggga 540

aaaaacagca aattccttaa ttttggtaat ttttattctt ggtctttttg ttcttggaat 600

cgccagcata ctctattact attttttca atg gaa gca gca agt tta agt ctc   652
                                    Met Glu Ala Ala Ser Leu Ser Leu
                                    1   5

tcc aat ctt tgg ttt gga ttc ttg ctt ggc ctc cta tgt ttt ctt gat   700
Ser Asn Leu Trp Phe Gly Phe Leu Leu Gly Leu Leu Cys Phe Leu Asp
    10   15   20

aat tca tcc ttt aaa aat gat gta aaa gaa gaa tca acc aaa tat ttg   748
Asn Ser Ser Phe Lys Asn Asp Val Lys Glu Glu Ser Thr Lys Tyr Leu

```
        25                    30                    35                    40

ctt cta aca tcc ata gtg tta agg ata ttg tgc tct ctg gtg gag aga    796
Leu Leu Thr Ser Ile Val Leu Arg Ile Leu Cys Ser Leu Val Glu Arg
                      45                    50                    55

att tct ggt tat gtc cgt cat cgg ccc act tta cta acc aca gtt gaa    844
Ile Ser Gly Tyr Val Arg His Arg Pro Thr Leu Leu Thr Thr Val Glu
                      60                    65                    70

ttt ctg gag ctt gtt gga ttt gcc att gcc agc aca act atg ttg gtg    892
Phe Leu Glu Leu Val Gly Phe Ala Ile Ala Ser Thr Thr Met Leu Val
                      75                    80                    85

gag aag tct ctg agt gtc att ttg ctt gtt gta gct ctg gct atg ctg    940
Glu Lys Ser Leu Ser Val Ile Leu Leu Val Val Ala Leu Ala Met Leu
         90                    95                   100

att att gat ctg aga atg aaa tct ttc tta gct att cca aac tta gtt    988
Ile Ile Asp Leu Arg Met Lys Ser Phe Leu Ala Ile Pro Asn Leu Val
105                   110                   115                   120

att ttt gca gtt ttg tta ttt ttt tcc tca ttg gaa act ccc aaa aat    1036
Ile Phe Ala Val Leu Leu Phe Phe Ser Ser Leu Glu Thr Pro Lys Asn
                      125                   130                   135

ccg att gct ttt gcg tgt ttt ttt att tgc ctg ata act gat cct ttc    1084
Pro Ile Ala Phe Ala Cys Phe Phe Ile Cys Leu Ile Thr Asp Pro Phe
                      140                   145                   150
```

出証特２００２－３０３２９３５

```
ctt gac att tat ttt agt gga ctt tca gta act gaa aga tgg aaa ccc    1132
Leu Asp Ile Tyr Phe Ser Gly Leu Ser Val Thr Glu Arg Trp Lys Pro
        155                 160                 165


ttt ttg tac cgt gga aga att tgc aga aga ctt tca gtc gtt ttt gct    1180
Phe Leu Tyr Arg Gly Arg Ile Cys Arg Arg Leu Ser Val Val Phe Ala
        170                 175                 180


gga atg att gag ctt aca ttt ttt att ctt tcc gca ttc aaa ctt aga    1228
Gly Met Ile Glu Leu Thr Phe Phe Ile Leu Ser Ala Phe Lys Leu Arg
185                 190                 195                 200


gac act cac ctc tgg tat ttt gta ata cct ggc ttt tcc att ttt gga    1276
Asp Thr His Leu Trp Tyr Phe Val Ile Pro Gly Phe Ser Ile Phe Gly
                205                 210                 215


att ttc tgg atg att tgt cat att att ttt ctt tta act ctt tgg gga    1324
Ile Phe Trp Met Ile Cys His Ile Ile Phe Leu Leu Thr Leu Trp Gly
                220                 225                 230


ttc cat acc aaa tta aat gac tgc cat aaa gta tat ttt act cac agg    1372
Phe His Thr Lys Leu Asn Asp Cys His Lys Val Tyr Phe Thr His Arg
                235                 240                 245


aca gat tac aat agc ctt gat aga atc atg gca tcc aaa ggg atg cgc    1420
Thr Asp Tyr Asn Ser Leu Asp Arg Ile Met Ala Ser Lys Gly Met Arg
        250                 255                 260
```

```
cat ttt tgc ttg att tca gag cag ttg gtg ttc ttt agt ctt ctt gca      1468
His Phe Cys Leu Ile Ser Glu Gln Leu Val Phe Phe Ser Leu Leu Ala
265             270             275             280


aca gcg att ttg gga gca gtt tcc tgg cag cca aca aat gga att ttc      1516
Thr Ala Ile Leu Gly Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe
                285             290             295


ttg agc atg ttt cta atc gtt ttg cca ttg gaa tcc atg gct cat ggg      1564
Leu Ser Met Phe Leu Ile Val Leu Pro Leu Glu Ser Met Ala His Gly
                300             305             310


ctc ttc cat gaa ttg ggt aac tgt tta gga gga aca tct gtt gga tat      1612
Leu Phe His Glu Leu Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr
                315             320             325


gct att gtg att ccc acc aac ttc tgc agt cct gat ggt cag cca aca      1660
Ala Ile Val Ile Pro Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr
                330             335             340


ctg ctt ccc cca gaa cat gta cag gag tta aat ttg agg tct act ggc      1708
Leu Leu Pro Pro Glu His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly
345             350             355             360


atg ctc aat gct atc caa aga ttt ttt gca tat cat atg att gag acc      1756
Met Leu Asn Ala Ile Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr
                365             370             375


tat gga tgt gac tat tcc aca agt gga ctg tca ttt gat act ctg cat      1804
```

Tyr Gly Cys Asp Tyr Ser Thr Ser Gly Leu Ser Phe Asp Thr Leu His
        380   385   390

tcc aaa cta aaa gct ttc ctc gaa ctt cgg aca gtg gat gga ccc aga   1852
Ser Lys Leu Lys Ala Phe Leu Glu Leu Arg Thr Val Asp Gly Pro Arg
        395   400   405

cat gat acg tat att ttg tat tac agt ggg cac acc cat ggt aca gga   1900
His Asp Thr Tyr Ile Leu Tyr Tyr Ser Gly His Thr His Gly Thr Gly
        410   415   420

gag tgg gct cta gca ggt gga gat aca cta cgc ctt gac aca ctt ata   1948
Glu Trp Ala Leu Ala Gly Gly Asp Thr Leu Arg Leu Asp Thr Leu Ile
425   430   435   440

gaa tgg tgg aga gaa aag aat ggt tcc ttt tgt tcc cgg ctt att atc   1996
Glu Trp Trp Arg Glu Lys Asn Gly Ser Phe Cys Ser Arg Leu Ile Ile
            445   450   455

gta tta gac agc gaa aat tca acc cct tgg gtg aaa gaa gtg agg aaa   2044
Val Leu Asp Ser Glu Asn Ser Thr Pro Trp Val Lys Glu Val Arg Lys
        460   465   470

att aat gac cag tat att gca gtg caa gga gca gag ttg ata aaa aca   2092
Ile Asn Asp Gln Tyr Ile Ala Val Gln Gly Ala Glu Leu Ile Lys Thr
        475   480   485

gta gat att gaa gaa gct gac ccg cca cag cta ggt gac ttt aca aaa   2140
Val Asp Ile Glu Glu Ala Asp Pro Pro Gln Leu Gly Asp Phe Thr Lys

```
              490                495               500


gac tgg gta gaa tat aac tgc aac tcc agt aat aac atc tgc tgg act   2188
Asp Trp Val Glu Tyr Asn Cys Asn Ser Ser Asn Asn Ile Cys Trp Thr
505             510             515             520


gaa aag gga cgc aca gtg aaa gca gta tat ggt gtg tca aaa cgg tgg   2236
Glu Lys Gly Arg Thr Val Lys Ala Val Tyr Gly Val Ser Lys Arg Trp
                525             530             535


agt gac tac act ctg cat ttg cca acg gga agc gat gtg gcc aag cac   2284
Ser Asp Tyr Thr Leu His Leu Pro Thr Gly Ser Asp Val Ala Lys His
                540             545             550


tgg atg tta cac ttt cct cgt att aca tat ccc cta gtg cat ttg gca   2332
Trp Met Leu His Phe Pro Arg Ile Thr Tyr Pro Leu Val His Leu Ala
                555             560             565


aat tgg tta tgc ggt ctg aac ctt ttt tgg atc tgc aaa act tgt ttt   2380
Asn Trp Leu Cys Gly Leu Asn Leu Phe Trp Ile Cys Lys Thr Cys Phe
                570             575             580


agg tgc ttg aaa aga tta aaa atg agt tgg ttt ctt cct act gtg ctg   2428
Arg Cys Leu Lys Arg Leu Lys Met Ser Trp Phe Leu Pro Thr Val Leu
585             590             595             600


gac aca gga caa ggc ttc aaa ctt gtc aaa tct taatttggac cccaaagcgg 2481
Asp Thr Gly Gln Gly Phe Lys Leu Val Lys Ser
                605             610
```

gatattaata agcactcata ctaccaatta tcactaactt gccattttt gtatgctgta 2541

ttttatttg tggaaaatac cttgctactt ctgtagctgc tctcactttg tcttttctta 2601

agtaattatg gtatatataa ggcgttggga aaaaacattt tataatgaaa gtatgtaggg 2661

agtcaaatgc ttactgtaaa tgcataagag acgttaaaaa taacactgca ctttcaggaa 2721

tgtttgctta tggtcctgat tagaaagaaa cagttgtcta tgctctgcaa tggtcaatga 2781

tgaattacta atgccttatt ttctaggcat ataataatag tttagagaat gtagaccaga 2841

taaatttgtt tactgtttta agaaaactac cagtttactt acagaagatt cttttttcca 2901

aacagtaggt ttcatccaag accatttgaa gaactgcaaa ctctttctct tagaaaagaa 2961

agagggcagc ctaaaataaa cgcaaaattt gcttatactc catcac 3007

<210> 81

<211> 184

<212> PRT

<213> Homo sapiens

<400> 81

Met Thr Ser Phe Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu

1   5   10   15

Gln Met Thr Val Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln
　　　　　　　 20　　　　　　　　　 25　　　　　　　　 30

Ser Ile Ser Phe Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys
　　　　 35　　　　　　　　　 40　　　　　　　　　 45

Phe Gly Arg Asn Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln
　　　　 50　　　　　　　　　 55　　　　　　　　　 60

Val Ser Arg Val Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser
65　　　　　　　　　 70　　　　　　　　 75　　　　　　　　　 80

Ser Val Leu Ser Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu
　　　　　　　 85　　　　　　　　　 90　　　　　　　　　 95

Ile Val Asp Ser Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro
　　　　　　 100　　　　　　　　 105　　　　　　　　 110

Tyr Arg Cys Met Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys
　　　　　 115　　　　　　　　 120　　　　　　　　 125

Glu Asp Gly Glu Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser
　　　　　 130　　　　　　　　 135　　　　　　　　 140

Pro Arg Ser Leu Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile
145　　　　　　　　 150　　　　　　　　 155　　　　　　　 160

Pro Glu Tyr Gly Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro
　　　　　　 165　　　　　　　　 170　　　　　　　　 175

Thr Glu Met Asp Glu Asn Glu Ser
180

<210> 82

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (285)..(836)

<400> 82

tttttacaaa ggccccgggc gcgagaggac gtgctctgcc agccagtggg aaggcaggcc 60

gcgcgcgcgg gagcgcggga ggatcggcgg ctcgcggtca ctggtccctg gctcggttcc 120

ccgcaccccg gggctcacac ttacccgcgc ggaggagcag cggccgggtg tccaccccca 180

tcctgcgccc agtctcctcg attcccctcg ctctgagccg ggagagccga acagctgaag 240

agagttcact gactccccag ccccaggtgg gccttgtgca catc atg acc agt ttt 296

　　　　　　　　　　　　　　　　　　　　　　　　　　　Met Thr Ser Phe

　　　　　　　　　　　　　　　　　　　　　　　　　　　1

gaa gat gct gac aca gaa gag aca gta act tgt ctc cag atg acg gtt 344

Glu Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val

	5				10					15					20	

tac cat cct ggc cag ttg cag tgt gga ata ttt cag tca ata agt ttt　392
Tyr His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe
　　　　　　　　　　　25　　　　　　　　　30　　　　　　　　　35

aac aga gag aaa ctc cct tcc agc gaa gtg gtg aaa ttt ggc cga aat　440
Asn Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn
　　　　　　　40　　　　　　　　　45　　　　　　　　　50

tcc aac atc tgt cat tat act ttt cag gac aaa cag gtt tcc cga gtt　488
Ser Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val
　　　　　　　55　　　　　　　　　60　　　　　　　　　65

cag ttt tct ctg cag ctg ttt aaa aaa ttc aac agc tca gtt ctc tcc　536
Gln Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser
　　　　70　　　　　　　　　75　　　　　　　　　80

ttt gaa ata aaa aat atg agt aaa aag acc aat ctg atc gtg gac agc　584
Phe Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser
　85　　　　　　　　　90　　　　　　　　　95　　　　　　　　　100

aga gag ctg ggc tac cta aat aaa atg gac ctg cca tac agg tgc atg　632
Arg Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met
　　　　　　　105　　　　　　　　　110　　　　　　　　　115

gtc aga ttc gga gag tat cag ttt ctg atg gag aag gaa gat ggc gag　680
Val Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu
　　　　　　　120　　　　　　　　　125　　　　　　　　　130

```
tca ttg gaa ttt ttt gag act caa ttt att tta tct cca aga tca ctc   728
Ser Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu
        135                 140                 145


ttg caa gaa aac aac tgg cca cca cac agg ccc ata ccg gag tat ggc   776
Leu Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly
        150                 155                 160


act tat tcg ctc tgc tcc tcc caa agc agt tct ccg aca gaa atg gat   824
Thr Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp
165                 170                 175                 180


gaa aat gag tca tgaacacaga aagtctaaga ggagaaatat gatggatgaa        876
Glu Asn Glu Ser


gagctctgta gatgctgtat agacactaaa taagagttga ttagggtagt atattatagt 936


catctgttat gctgtgaaat ttggaattca gtattatcat tttgaagtct gtaaattgtg 996


ttagtcatta acttagtcac ctgttgtatt ctggatctac acaaaattat tttaactgct 1056


cttattaatc tgtgaggatt aatatacaaa aagtatcctt tgagatgaag tcgtgttctc 1116


aaaataaggt tatattattt tctttttctg cttgattttc atcttgtgtt ttgctttgtt 1176


tttgtaagga accatctctt ggtttggtca catcagttca caacagccat ttgttttcaa 1236


ggtcaaggct ccaggcaggt tgttactggt gtttgcagcc tgtcagtact tgcagtactg 1296
```

gaataggttc taggctagtg tctgcgcgtc actgtggttt tagcatggga ggacttattt 1356

gagaaatact accttacttt tctatgattt cttttttacag agttatagtg tgtttactcc 1416

taagatgaca gttctctttg tctatattca gcatctaaga caaatattta aacattttaa 1476

agaaccactg tgttaagttt aggattattt acttaccaaa ttagaagttt gacttttatg 1536

tgttatacac aatcttaaaa tttcacgaat tcacctttttt aatagtatcc atgtacataa 1596

taaaatcaaa gtttaattag c 1617

<210> 83

<211> 392

<212> PRT

<213> Homo sapiens

<400> 83

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1   5   10   15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
            20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
        35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
　　　 50　　　　　　　　　 55　　　　　　　　 60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
　　 65　　　　　　　　 70　　　　　　　　 75　　　　　　　　 80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
　　　　　　　　　 85　　　　　　　　 90　　　　　　　　 95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
　　　　　　　 100　　　　　　　 105　　　　　　　 110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
　　　　　 115　　　　　　　 120　　　　　　　 125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
　　　　 130　　　　　　　 135　　　　　　　 140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145　　　　　　　 150　　　　　　　 155　　　　　　　 160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
　　　　　　　 165　　　　　　　 170　　　　　　　 175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
　　　　　　 180　　　　　　　 185　　　　　　　 190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
　　　　　 195　　　　　　　 200　　　　　　　 205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245   250   255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
            260   265   270

Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
            275   280   285

Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
    290   295   300

Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305   310   315   320

Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                325   330   335

Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
                340   345   350

Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg

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                355                   360                   365
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Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
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                370                   375                   380
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Val Glu Ser Pro Val Gln Lys Val
```
                385                   390
```


<210> 84

<211> 1898

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1294)

<400> 84

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acttccgctg gccgctggct cgctggccgc tcctggaggc ggcggcggga gcgcaggggg  60
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cgcgcggccc ggggactcgc attccccggt tccccctcca ccccacgcgg cctggacc    118
```

```
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc  166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
 1               5                  10                  15
```

```
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc  214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
```

```
               20                    25                    30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc    262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
               35                    40                    45


ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac    310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
               50                    55                    60


tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt    358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
   65                    70                    75                    80


gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc    406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                         85                    90                    95


cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg    454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
               100                   105                   110


ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg    502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
               115                   120                   125


ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca    550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
               130                   135                   140
```

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ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga   598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145             150             155             160


gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag   646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165             170             175


ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc   694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                180             185             190


aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc   742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
                195             200             205


ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg   790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
                210             215             220


ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac   838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225             230             235             240


ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc   886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245             250             255
```

```
agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc    934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
            260                 265                 270


ttc aca gtg ggc tca ctg cta gaa cag ggg gcc cta ctg gag gga acc    982
Phe Thr Val Gly Ser Leu Leu Glu Gln Gly Ala Leu Leu Glu Gly Thr
            275                 280                 285


cgc ttc atg ggg cga cac agt gag ttt gct gcc cat gcc ctg cta ctc   1030
Arg Phe Met Gly Arg His Ser Glu Phe Ala Ala His Ala Leu Leu Leu
        290                 295                 300


tcc atc tgc tcc gca tgt ggc cag ctc ttc atc ttt tac acc att ggg   1078
Ser Ile Cys Ser Ala Cys Gly Gln Leu Phe Ile Phe Tyr Thr Ile Gly
305                 310                 315                 320


cag ttt ggg gct gcc gtc ttc acc atc atc atg acc ctc cgc cag gcc   1126
Gln Phe Gly Ala Ala Val Phe Thr Ile Ile Met Thr Leu Arg Gln Ala
                325                 330                 335


ttt gcc atc ctt ctt tcc tgc ctt ctc tat ggc cac act gtc act gtg   1174
Phe Ala Ile Leu Leu Ser Cys Leu Leu Tyr Gly His Thr Val Thr Val
            340                 345                 350


gtg gga ggg ctg ggg gtg gct gtg gtc ttt gct gcc ctc ctg ctc aga   1222
Val Gly Gly Leu Gly Val Ala Val Val Phe Ala Ala Leu Leu Leu Arg
            355                 360                 365


gtc tac gcg cgg ggc cgt cta aag caa cgg gga aag aag gct gtg cct   1270
Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
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Val Tyr Ala Arg Gly Arg Leu Lys Gln Arg Gly Lys Lys Ala Val Pro
   370   375   380

gtt gag tct cct gtg cag aag gtt tgagggtgga aagggcctga ggggtgaagt   1324
Val Glu Ser Pro Val Gln Lys Val
   385   390

gaaataggac cctcccacca tccccttctg ctgtaacctc tgagggagct ggctgaaagg   1384

gcaaaatgca ggtgttttct cagtatcaca gaccagctct gcagcagggg attggggagc   1444

ccaggaggca gccttccctt ttgccttaag tcacccatct tccagtaagc agtttattct   1504

gagccccggg ggtagacagt cctcagtgag gggttttggg gagtttgggg tcaagagagc   1564

ataggtaggt tccacagtta ctcttcccac aagttccctt aagtcttgcc ctagctgtgc   1624

tctgccacct tccagactca ctccctctg caaatacctg catttcttac cctggtgaga   1684

aaagcacaag cggtgtaggc tccaatgctg ctttcccagg agggtgaaga tggtgctgtg   1744

ctgaggaaag gggatgcaga gccctgccca gcaccaccac ctcctatgct cctggatccc   1804

taggctctgt tccatgagcc tgttgcaggt tttggtactt tagaaatgta actttttgct   1864

cttataattt tattttatta aattaaatta ctgc   1898

<210> 85

<211> 432

<212> PRT

<213> Homo sapiens

<400> 85

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser

1   5   10   15

Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr

                20   25   30

Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser

                35   40   45

Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn

        50   55   60

Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys

65   70   75   80

Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro

                85   90   95

Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu

                100   105   110

Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val

                115   120   125

Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
    130   135   140

Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145   150   155   160

Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
                165   170   175

Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
                180   185   190

Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
                195   200   205

Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
    210   215   220

Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225   230   235   240

Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245   250   255

Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
                260   265   270

Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
                275   280   285

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
    290   295   300

Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305   310   315   320

Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
                325   330   335

Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
                340   345   350

Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
        355   360   365

Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
    370   375   380

Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385   390   395   400

Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys
                405   410   415

Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
                420   425   430

<210> 86

<211> 2018

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1414)

<400> 86

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cgcgcggccc ggggactcgc attccccggt tcccccctcca ccccacgcgg cctggacc    118

atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc     166
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
1               5                   10                  15

cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc     214
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
                20                  25                  30

cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc     262
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
            35                  40                  45

ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac     310
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
        50                  55                  60
```

```
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt    358
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
 65                 70              75                  80


gtg ttt ggc aat gag ccc aag gcc tct gat gag gtt ccc ctg gcg ccc    406
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
                85              90              95


cga aca gag gcg gca gag acc acc ccg atg tgg cag gcc ctg aag ctg    454
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
            100             105             110


ctc ttc tgt gcc aca ggg ctc cag gtg tct tat ctg act tgg ggt gtg    502
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
            115             120             125


ctg cag gaa aga gtg atg acc cgc agc tat ggg gcc aca gcc aca tca    550
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
        130             135             140


ccg ggt gag cgc ttt acg gac tcg cag ttc ctg gtg cta atg aac cga    598
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
145             150             155             160


gtg ctg gca ctg att gtg gct ggc ctc tcc tgt gtt ctc tgc aag cag    646
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
            165             170             175
```

```
ccc cgg cat ggg gca ccc atg tac cgg tac tcc ttt gcc agc ctg tcc    694
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
            180                 185                 190


aat gtg ctt agc agc tgg tgc caa tac gaa gct ctt aag ttc gtc agc    742
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
            195                 200                 205


ttc ccc acc cag gtg ctg gcc aag gcc tct aag gtg atc cct gtc atg    790
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
            210                 215                 220


ctg atg gga aag ctt gtg tct cgg cgc agc tac gaa cac tgg gag tac    838
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
225                 230                 235                 240


ctg aca gcc acc ctc atc tcc att ggg gtc agc atg ttt ctg cta tcc    886
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser
                245                 250                 255


agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc    934
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu
            260                 265                 270


atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg    982
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp
            275                 280                 285


cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt   1030
```

Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe
    290   295   300

ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa   1078
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu
305   310   315   320

cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag   1126
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu
                    325   330   335

ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag   1174
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln
                    340   345   350

ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc   1222
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr
                    355   360   365

atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt   1270
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu
    370   375   380

ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg   1318
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val
385   390   395   400

gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag   1366
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys

405   410   415

```
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt   1414
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val
```

    420   425   430

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tgagggtgga aagggcctga ggggtgaagt gaaataggac cctcccacca tcccttctg   1474

ctgtaacctc tgagggagct ggctgaaagg gcaaaatgca ggtgttttct cagtatcaca   1534

gaccagctct gcagcagggg attggggagc ccaggaggca gccttccctt ttgccttaag   1594

tcacccatct tccagtaagc agtttattct gagccccggg ggtagacagt cctcagtgag   1654

gggttttggg gagtttgggg tcaagagagc ataggtaggt tccacagtta ctcttcccac   1714

aagttccctt aagtcttgcc ctagctgtgc tctgccacct tccagactca ctccctctg   1774

caaatacctg catttcttac cctggtgaga aaagcacaag cggtgtaggc tccaatgctg   1834

ctttcccagg agggtgaaga tggtgctgtg ctgaggaaag gggatgcaga gccctgccca   1894

gcaccaccac ctcctatgct cctggatccc taggctctgt tccatgagcc tgttgcaggt   1954

tttggtactt tagaaatgta actttttgct cttataattt tattttatta aattaaatta   2014

ctgc                                                               2018
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<210> 87

<211> 235

<212> PRT

<213> Homo sapiens

<400> 87

Met Gly Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser

1   5   10   15

Trp Gly Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser

                     20   25   30

Asp Ser Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His

                35   40   45

Ser Asn Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser

           50   55   60

Val Glu Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys

65   70   75   80

Phe Val Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val

                85   90   95

Gln Asn Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe

                100   105   110

Ala Glu Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala

                115   120   125

Val Asn Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu
    130   135   140

Arg Asp Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser
145   150   155   160

Val Asn Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu
                165   170   175

Asn Asn Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile
            180   185   190

Asn Ala Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg
        195   200   205

Ile Phe Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu
    210   215   220

Thr Arg Asn Met Val Gln Arg Gln Phe Ile Ala
225   230   235

<210> 88

<211> 2717

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (111)..(815)

<400> 88

aaaaggaaga cagaaaagcc gcgggctgac tgtggtggcg ctcgcctgca gattgaaaag 60

aaatgctgag aaatacataa agttttcctc ttctgccttg gatatttata atg ggt 116
                                                           Met Gly
                                                             1

atc ggg aag tct aaa ata aat tcc tgc cct ctt tct ctc tct tgg ggt 164
Ile Gly Lys Ser Lys Ile Asn Ser Cys Pro Leu Ser Leu Ser Trp Gly
          5   10   15

aaa agg cac agt gtg gat aca agt cca gga tat cat gag tca gat tcc 212
Lys Arg His Ser Val Asp Thr Ser Pro Gly Tyr His Glu Ser Asp Ser
  20   25   30

aag aag tct gaa gat cta tcc ttg tgt aat gtt gct gag cac agc aat 260
Lys Lys Ser Glu Asp Leu Ser Leu Cys Asn Val Ala Glu His Ser Asn
35   40   45   50

aca aca gag ggg cca aca gga aag cag gag gga gct cag agc gtg gaa 308
Thr Thr Glu Gly Pro Thr Gly Lys Gln Glu Gly Ala Gln Ser Val Glu
             55   60   65

gag atg ttt gaa gaa gaa gct gaa gaa gag gtg ttc ctc aaa ttt gtg 356
Glu Met Phe Glu Glu Glu Ala Glu Glu Glu Val Phe Leu Lys Phe Val
             70   75   80

```
ata ttg cat gca gaa gat gac aca gat gaa gcc ctc aga gtc cag aat    404
Ile Leu His Ala Glu Asp Asp Thr Asp Glu Ala Leu Arg Val Gln Asn
            85              90              95


ctg cta caa gat gac ttt ggt atc aaa ccc gga ata atc ttt gct gag    452
Leu Leu Gln Asp Asp Phe Gly Ile Lys Pro Gly Ile Ile Phe Ala Glu
        100             105             110


atg cca tgt ggc aga cag cat tta cag aat tta gat gat gct gta aat    500
Met Pro Cys Gly Arg Gln His Leu Gln Asn Leu Asp Asp Ala Val Asn
115             120             125             130


ggg tct gca tgg aca atc tta tta ctg act gaa aac ttt tta aga gat    548
Gly Ser Ala Trp Thr Ile Leu Leu Leu Thr Glu Asn Phe Leu Arg Asp
            135             140             145


act tgg tgt aat ttc cag ttc tat acg tcc cta atg aac tcc gtt aac    596
Thr Trp Cys Asn Phe Gln Phe Tyr Thr Ser Leu Met Asn Ser Val Asn
            150             155             160


agg cag cat aaa tac aac tct gtt ata ccc atg cgg ccc ctg aac aat    644
Arg Gln His Lys Tyr Asn Ser Val Ile Pro Met Arg Pro Leu Asn Asn
            165             170             175


ccc ctt ccc cga gaa agg act ccc ttt gcc ctc caa acc atc aat gcc    692
Pro Leu Pro Arg Glu Arg Thr Pro Phe Ala Leu Gln Thr Ile Asn Ala
        180             185             190
```

tta gag gaa gaa agt cgt gga ttt cct aca caa gta gaa aga att ttt　　740
Leu Glu Glu Glu Ser Arg Gly Phe Pro Thr Gln Val Glu Arg Ile Phe
195　　　　　　　200　　　　　　　205　　　　　　　210

cag gag tct gtg tat aag aca caa caa act ata tgg aaa gag aca aga　　788
Gln Glu Ser Val Tyr Lys Thr Gln Gln Thr Ile Trp Lys Glu Thr Arg
　　　　　　　215　　　　　　　220　　　　　　　225

aat atg gta caa aga caa ttt att gcc tgagatgaaa catataacat　　835
Asn Met Val Gln Arg Gln Phe Ile Ala
　　　　　　　230　　　　　　　235

gtggctggct cttgttttgt aaaccaaatg attaatcttc acttgagaaa gcagtttcta 895

ggaaatgttt aaataaaaga gagtcttcac cttaaagaaa cctatggagc acaagaaaga 955

taaatttctg caggacagcc tataaaattg tggtactttt tgatgtttca gtaaacttga 1015

cattgtcaga gtttcaagga cttttctttc acaattttcc tagttcatgg atatgaaaaa 1075

ggaattctca atccatattc cttgtattga accttgaaca aaaacttgta tgacagacat 1135

ttttaaaaat gtgacaacac ttttattctc tgaattttga tctcaaagga cacagaaaaa 1195

aaatggcccc aggagatctg atcacacttc ctcctgaggc acctctcatg gatgttgcaa 1255

taagcattcg ggtactatca cccagaaata tgaattgcca gaatagaaca tttagcatgt 1315

taagcgttga tgcatataaa atcagaaata gatgtgagaa tggtggaact ttttaaaaga 1375

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acccagtcaa atgtattttc tgctgaaatc tgcatatttg gaggcatttc ccaccaccga 1435

ttcacagccc atttgatagt gtggtagtta gggacttcgt ggagtggtgt tcagacgtcc 1495

cctggggctt aaatctcttc atattagtca tcatttgtaa ctatggcttt atttgcagag 1555

cttctaaaag gcgtataact gtgtgagtgg ccagatattc acttttttaga tcaaaaacct 1615

ctcttatgga agctttaaaa gtttccgtca cacacaattc tcttctcagg aagtatttct 1675

catttaggtc ttcaaagtag cctgactgtg tgcatgtgtg tgtgtgatag gttatttata 1735

aagactttgg atagaaggag atgtatttta ttacctccta ttctagagcc ccatgctcct 1795

aacaagccag agaggcccca aacaggattg tttctttcct ccacagccct tctgcccatc 1855

tgagattgag ggagcatcgt ccacttgaga tcagggatgg ggtggagaat gggtcatgtc 1915

atgtaatgag aaaagccctc ttcgggatca tgagacttgg ttctagtcca atttctgcca 1975

ctgaggatga atgtaactgt gggcaaacta tttaccctcc tttatctgtg aaatgaaagg 2035

gttgaattga tggatctcta aaggcttttg tcctctatga ggatgtgaaa aactagggac 2095

cacaaaaggg aacaagcaaa aaagtttgga ttcgataaag tgatatgtaa tagttgcaga 2155

aggctttata tatgcttata atgaaaagat attttttgta tattgacagc ataatttatt 2215
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tttaatgctg tcattacact taaagtcaca ggaaaaaaat atacatgctt actcaggctt 2275

tcttaaaaat aaatttttat agagatcctt gagtaaagac attttgctta atttcttttt 2335

tcttattccc cacttgtata tcccctacca gtaccgggat ctgcacacat cttttttgcag 2395

ttacctcttc atagccatga accaaaacgt tctatgagga gcatgcaagt aagtcaagcc 2455

tcctattctg ttagtactta ttagaggagg agatggtttt cattgcatag tgacattttc 2515

ttagccttaa cgttctgata gtagcttact actcacttct cttttttcagt tttcataata 2575

agtattcatt tttttgccat aatgcttcct gtaaagccaa ttttatatac taataaaaca 2635

tgaactgccc actcttcatg cctgccaaac ttggggcaat tgatgctaaa tggtattttt 2695

aaaataaatg tttttattct tt                                          2717
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<210> 89

<211> 245

<212> PRT

<213> Homo sapiens

<400> 89

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Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
1               5                   10                  15
```

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Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
```

```
            20                    25                    30
```

Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn

```
      35                    40                    45
```

Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu

```
      50                    55                    60
```

Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe

```
  65                    70                    75                    80
```

Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe

```
                  85                    90                    95
```

Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe

```
                  100                   105                   110
```

Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys

```
                  115                   120                   125
```

Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val

```
                  130                   135                   140
```

Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg

```
  145                   150                   155                   160
```

Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser

```
                  165                   170                   175
```

Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
        180   185   190

Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
        195   200   205

Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
        210   215   220

Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225   230   235   240

Gln Tyr Glu Ile Val
        245

<210> 90

<211> 1793

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (60)..(794)

<400> 90

gcgtctcgct ctctgtgttc caatcgcccg gtgcggtggt gcagggtctc gggctagtc   59

atg gcg tcc ccg tct cgg aga ctg cag act aaa cca gtc att act tgt   107

```
    Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr Cys
    1                   5                   10                  15


    ttc aag agc gtt ctg cta atc tac act ttt att ttc tgg atc act ggc    155
    Phe Lys Ser Val Leu Leu Ile Tyr Thr Phe Ile Phe Trp Ile Thr Gly
                    20                  25                  30


    gtt atc ctt ctt gca gtt ggc att tgg ggc aag gtg agc ctg gag aat    203
    Val Ile Leu Leu Ala Val Gly Ile Trp Gly Lys Val Ser Leu Glu Asn
                    35                  40                  45


    tac ttt tct ctt tta aat gag aag gcc acc aat gtc ccc ttc gtg ctc    251
    Tyr Phe Ser Leu Leu Asn Glu Lys Ala Thr Asn Val Pro Phe Val Leu
                50                  55                  60


    att gct act ggt acc gtc att att ctt ttg ggc acc ttt ggt tgt ttt    299
    Ile Ala Thr Gly Thr Val Ile Ile Leu Leu Gly Thr Phe Gly Cys Phe
    65                  70                  75                  80


    gct acc tgc cga gct tct gca tgg atg cta aaa ctg tat gca atg ttt    347
    Ala Thr Cys Arg Ala Ser Ala Trp Met Leu Lys Leu Tyr Ala Met Phe
                    85                  90                  95


    ctg act ctc gtt ttt ttg gtc gaa ctg gtc gct gcc atc gta gga ttt    395
    Leu Thr Leu Val Phe Leu Val Glu Leu Val Ala Ala Ile Val Gly Phe
                    100                 105                 110


    gtt ttc aga cat gag att aag aac agc ttt aag aat aat tat gag aag    443
    Val Phe Arg His Glu Ile Lys Asn Ser Phe Lys Asn Asn Tyr Glu Lys
```

出証特２００２－３０３２９３５

```
               115                    120                    125

gct ttg aag cag tat aac tct aca gga gat tat aga agc cat gca gta    491
Ala Leu Lys Gln Tyr Asn Ser Thr Gly Asp Tyr Arg Ser His Ala Val
     130                    135                    140

gac aag atc caa aat acg ttg cat tgt tgt ggt gtc acc gat tat aga    539
Asp Lys Ile Gln Asn Thr Leu His Cys Cys Gly Val Thr Asp Tyr Arg
     145                    150                    155                    160

gat tgg aca gat act aat tat tac tca gaa aaa gga ttt cct aag agt    587
Asp Trp Thr Asp Thr Asn Tyr Tyr Ser Glu Lys Gly Phe Pro Lys Ser
                    165                    170                    175

tgc tgt aaa ctt gaa gat tgt act cca cag aga gat gca gac aaa gta    635
Cys Cys Lys Leu Glu Asp Cys Thr Pro Gln Arg Asp Ala Asp Lys Val
                    180                    185                    190

aac aat gaa ggt tgt ttt ata aag gtg atg acc att ata gag tca gaa    683
Asn Asn Glu Gly Cys Phe Ile Lys Val Met Thr Ile Ile Glu Ser Glu
               195                    200                    205

atg gga gtc gtt gca gga att tcc ttt gga gtt gct tgc ttc caa ctg    731
Met Gly Val Val Ala Gly Ile Ser Phe Gly Val Ala Cys Phe Gln Leu
     210                    215                    220

att gga atc ttt ctc gcc tac tgc ctc tct cgt gcc ata aca aat aac    779
Ile Gly Ile Phe Leu Ala Tyr Cys Leu Ser Arg Ala Ile Thr Asn Asn
225                    230                    235                    240
```

cag tat gag ata gtg taacccaatg tatctgtggg cctattcctc tctaccttta　834

Gln Tyr Glu Ile Val

　　　　　　　　　245

aggacattta gggtccccc tgtgaattag aaagttgctt ggctggagaa ctgacaacac 894

tacttactga tagaccaaaa aactacacca gtaggttgat tcaatcaaga tgtatgtaga 954

cctaaaacta caccaatagg ctgattcaat caagatccgt gctcgcagtg ggctgattca 1014

atcaagatgt atgtttgcta tgttctaagt ccaccttcta tcccattcat gttagatcgt 1074

tgaaaccctg tatccctctg aaacactgga agagctagta aattgtaaat gaagtaatac 1134

tgtgttcctc ttgactgtta tttttcttag taggggggcct ttggaaggca ctgtgaattt 1194

gctattttga tgtagtgtta caagatggaa aattgattcc tctgactttg ctattgatgt 1254

agtgtgatag aaaattcacc cctctgaact ggctccttcc cagtcaaggt tatctggttt 1314

gattgtataa tttgcaccaa gaagttaaaa tgttttatga ctctctgttc tgctgacagg 1374

cagagagtca cattgtgtaa tttaatttca gtcagtcaat agatggcatc cctcatcagg 1434

gttgccagat ggtgataaca gtgtaaggcc ttgggtctaa ggcatccacg actggaaggg 1494

actactgatg ttctgtgata catcaggttt cagcacacaa cttacatttc tttgcctcca 1554

```
aattgaggca tttattatga tgttcatact ttccctcttg tttgaaagtt tctaattatt 1614

aaatggtgtc ggaattgttg tattttcctt aggaattcag tggaacttat cttcattaaa 1674

tttagctggt accaggttga tatgacttgt caatattatg gtcaacttta agtcttagtt 1734

ttcgtttgtg cctttgatta ataagtataa ctcttataca ataaatactg ctttcctct  1793
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<210> 91

<211> 180

<212> PRT

<213> Homo sapiens

<400> 91

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Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1               5                   10                  15

Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
                20                  25                  30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
                35                  40                  45

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
                50                  55                  60

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
65                  70                  75                  80
```

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
           85   90   95

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
         100   105   110

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
         115   120   125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
    130   135   140

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
145   150   155   160

Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
         165   170   175

Ala Leu Leu Gln
        180

<210> 92

<211> 970

<212> DNA

<213> Homo sapiens

<220>

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<221> CDS

<222> (26)..(565)


<400> 92

ttttttcagct aaaggggaga tctgg atg gca tct act tcg tat gac tat tgc      52
                              Met Ala Ser Thr Ser Tyr Asp Tyr Cys
                               1               5


aga gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg      100
Arg Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly
 10              15              20              25


ata gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg      148
Ile Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu
                 30              35              40


att atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt      196
Ile Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu
                 45              50              55


cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag      244
Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu
                 60              65              70


ctg acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gct gcc      292
Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala
                 75              80              85


acc tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag      340
```

Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu
90   95   100   105

aag gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act   388
Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr
                110   115   120

aca tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg   436
Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu
                125   130   135

aga aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac   484
Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr
            140   145   150

tac ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg   532
Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala Pro Gln Leu Leu
        155   160   165

att gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 585
Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
170   175   180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 645

ttctgagcgg gtcatggggc aacacggtta gcggggagag cacggggtag ccggagaagg 705

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 765

ttgacccagg gctgtctccc tccagagcct ccctccggac aatgagtccc ccctcttgtc 825

tcccaccctg agattgggca tggggtgcgg tgtgggggggc atgtgctgcc tgttgttatg 885

ggtttttttt gcggggggggg ttgctttttt ctggggtctt tgagctccaa aaaataaaca 945

cttcctttga gggagagcac acctt   970

<210> 93

<211> 331

<212> PRT

<213> Homo sapiens

<400> 93

Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe
1   5   10   15

Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn
                20   25   30

Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu
            35   40   45

Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala
        50   55   60

Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp
65   70   75   80

Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile
                85   90   95

Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly
            100   105   110

Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly
            115   120   125

Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr
    130   135   140

Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala
145   150   155   160

Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser
                165   170   175

Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu
            180   185   190

Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser
            195   200   205

Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile
            210   215   220

Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr

225   230   235   240

Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala
                    245   250   255

Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr
                    260   265   270

Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu
                    275   280   285

Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu
                    290   295   300

Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln
305   310   315   320

Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His
                    325   330

<210> 94

<211> 2039

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (175)..(1167)

<400> 94

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cacactcttt caagagaagc ttccttgggt taagaaaaaa aacgaaccct tccagtcagg 120

tcagtgactg gagagctcca aggaaagtct ctcagtgacc tggctgctgg cacc atg 177
                                                              Met
                                                                1

gac tca gaa aag aaa cgc ttt act gaa gag gcc acc aaa tac ttc cgg 225
Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe Arg
            5   10   15

gag aga gtc agc cca gtg cat ctg caa atc ctg ctg act aac aat gaa 273
Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn Glu
        20   25   30

gcc tgg aag aga ttc gtg act gcg gct gaa ttg ccc agg gat gag gca 321
Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu Ala
    35   40   45

gat gct ctc tac gaa gct ctg aag aag ctt aga aca tat gca gct att 369
Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala Ile
50   55   60   65

gag gac gaa tat gtg cag cag aaa gat gag cag ttt agg gaa tgg ttt 417
Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp Phe
            70   75   80

ttg aaa gag ttt ccc caa gtc aag agg aag atc cag gag tcc ata gaa　　465
Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile Glu
　　　　　　　　85　　　　　　　　　90　　　　　　　　　95

aag ctt cgt gcc ctt gca aat ggt att gaa gag gtc cac aga ggc tgc　　513
Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly Cys
　　　　　　　100　　　　　　　　105　　　　　　　　110

acc atc tcc aac gtg gtg tcc agc tcc act ggc gct gcc tct ggc atc　　561
Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly Ile
　　　　115　　　　　　　　120　　　　　　　　125

atg tcc ctt gct ggt ctt gtt ttg gca cca ttt aca gca ggg acg agt　　609
Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr Ser
130　　　　　　　　135　　　　　　　　140　　　　　　　　145

ctg gcc ctt act gca gct ggg gta ggg ctg gga gca gcg tct gct gtg　　657
Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala Val
　　　　　　　150　　　　　　　　155　　　　　　　　160

act ggg atc acc acc agc atc gtg gag cac tca tac aca tca tca gca　　705
Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser Ala
　　　　　　　165　　　　　　　　170　　　　　　　　175

gaa gct gaa gcc agc agg ctg act gca acc agc att gac cga ttg aag　　753
Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu Lys
　　　　　　　180　　　　　　　　185　　　　　　　　190

gta ttt aag gaa gtt atg cgt gac atc aca ccc aac tta ctt tcc ctt   801
Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser Leu
    195   200   205

ctt aat aat tat tac gaa gcc aca caa acc att ggg agt gaa atc cgt   849
Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile Arg
210   215   220   225

gcc atc agg caa gcc aga gcc agg gcc cga ctc cct gtg acc acc tgg   897
Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr Trp
         230   235   240

cga atc tca gct gga agt ggt ggt caa gca gag aga acg att gca ggc   945
Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala Gly
         245   250   255

acc acc cgg gca gtg agc aga gga gcc cgg atc ctg agt gcg acc act   993
Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr Thr
         260   265   270

tca ggc atc ttc ctt gca ctg gat gtg gtc aac ctt gta tac gag tca   1041
Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu Ser
    275   280   285

aag cac ttg cat gag ggg gca aag tct gca tct gct gag gag ctg agg   1089
Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu Arg
290   295   300   305

cgg cag gct cag gag ctg gag gag aat cta atg gag ctc act cag atc   1137

          出証特２００２－３０３２９３５

Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln Ile
          310   315   320

tat cag cgt ctg aat cca tgc cat acc cac tgaccccaga ccagtgcagc   1187
Tyr Gln Arg Leu Asn Pro Cys His Thr His
          325   330

cagcagggga ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga 1247

taaagagggc aaggtaaagt ttatggagct gagtgttagt gactttggca tttctgtagc 1307

tgagcacagc aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat 1367

gctggagcct ggaataaggg aggagagggg actggagagt gtggggaata ggaagaagaa 1427

atttccttta gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc 1487

agcaatgaga aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac 1547

ttttggatac agcagaagaa acagcggctc cactaccgac ctgcccccgg ttcgatgtcc 1607

ttccaagaat gaagtctttc cctggtgatg gtcccctgcc ctgtctttcc agcatccact 1667

ctgtcttgtc ctcctggaag tgtatctcag tcagccagtg gcttcttgat gatggcggtg 1727

gaggtggtgg ttgtagtgtg atggatcccc tttaggttat ttaggggtat atgtcccctg 1787

cttgaaccct gaaggccagg taatgagcca tggccattgt ccccagctga ggaccaggtg 1847

tctctaaaaa cccaaacatc ctggagagta tgcgagaacc taccaagaaa aacagtctca 1907

ttactcatat acagcaggca aagagacaga aaattaactg aaaagcagtt tagagactgg 1967

gggaggccgg atctctagag ccatcctgct gagtgccctg tgtgtaagtc ctaataaact 2027

cacctactca cc   2039

<210> 95

<211> 407

<212> PRT

<213> Homo sapiens

<400> 95

Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
1   5   10   15

Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys
            20   25   30

Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
        35   40   45

Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
        50   55   60

Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65   70   75   80

出証特２００２－３０３２９３５

Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                85   90   95

His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
                100   105   110

Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
                115   120   125

Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
    130   135   140

Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145   150   155   160

Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
                165   170   175

Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
                180   185   190

Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
                195   200   205

Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
    210   215   220

Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys

225   230   235   240

Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
                245   250   255

Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
                260   265   270

Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
                275   280   285

Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
                290   295   300

Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305   310   315   320

Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
                325   330   335

Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
                340   345   350

Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
                355   360   365

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
                370   375   380

Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385   390   395   400

Val Cys Lys Tyr Lys Leu Leu
                405

<210> 96

<211> 1409

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (181)..(1401)

<400> 96

gctgtgcttg gcgcgtaccg tgcggtccct gtagttggag gacgggcggt cgcgcggcct 60

ttcccactag ccggagtagc ctctagttcg ttagtcaaaa cgtgaaaaaa aaagacctgc 120

tttgccctgg gaaatagtaa ccctgccaaa tacatcagct tgtaggagac agaggatgtg 180

atg gag ctg ctt gaa gaa gat ctc aca tgc cct att tgt tgt agt ctg   228
Met Glu Leu Leu Glu Glu Asp Leu Thr Cys Pro Ile Cys Cys Ser Leu
  1   5   10   15

ttt gat gat cca cgg gtt ttg cct tgc tcc cac aac ttc tgc aaa aaa   276
Phe Asp Asp Pro Arg Val Leu Pro Cys Ser His Asn Phe Cys Lys Lys

<pre>
                  20   25   30

tgc tta gaa ggt atc tta gaa ggg agt gtg cgg aat tcc ttg tgg aga   324
Cys Leu Glu Gly Ile Leu Glu Gly Ser Val Arg Asn Ser Leu Trp Arg
         35   40   45

cca gct cca ttc aag tgt cct aca tgc cgt aag gaa act tca gct act   372
Pro Ala Pro Phe Lys Cys Pro Thr Cys Arg Lys Glu Thr Ser Ala Thr
         50   55   60

gga att aat agc ctg cag gtt aat tac tcc ctg aag ggt att gtg gaa   420
Gly Ile Asn Ser Leu Gln Val Asn Tyr Ser Leu Lys Gly Ile Val Glu
65   70   75   80

aag tat aac aag atc aag atc tct ccc aaa atg cca gta tgc aaa gga   468
Lys Tyr Asn Lys Ile Lys Ile Ser Pro Lys Met Pro Val Cys Lys Gly
                  85   90   95

cac ttg ggg cag cct ctc aac att ttc tgc ctg act gat atg cag ctg   516
His Leu Gly Gln Pro Leu Asn Ile Phe Cys Leu Thr Asp Met Gln Leu
                  100   105   110

att tgt ggg atc tgt gct act cgt ggg gag cac acc aaa cat gtc ttc   564
Ile Cys Gly Ile Cys Ala Thr Arg Gly Glu His Thr Lys His Val Phe
                  115   120   125

tgt tct att gaa gat gcc tat gct cag gaa agg gat gcc ttt gag tcc   612
Cys Ser Ile Glu Asp Ala Tyr Ala Gln Glu Arg Asp Ala Phe Glu Ser
         130   135   140
</pre>

出証特2002-3032935

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ctc ttc cag agc ttt gag acc tgg cgt cgg gga gat gct ctt tct cgc    660
Leu Phe Gln Ser Phe Glu Thr Trp Arg Arg Gly Asp Ala Leu Ser Arg
145             150             155             160


ttg gat acc ttg gaa act agt aag agg aaa tcc cta cag tta ctg act    708
Leu Asp Thr Leu Glu Thr Ser Lys Arg Lys Ser Leu Gln Leu Leu Thr
                165             170             175


aaa gat tca gat aaa gtg aag gaa ttt ttt gag aag tta caa cac aca    756
Lys Asp Ser Asp Lys Val Lys Glu Phe Phe Glu Lys Leu Gln His Thr
                180             185             190


ctg gat caa aag aag aat gaa att ctg tct gac ttt gag acc atg aaa    804
Leu Asp Gln Lys Lys Asn Glu Ile Leu Ser Asp Phe Glu Thr Met Lys
                195             200             205


ctt gct gtt atg caa gca tat gac cca gag atc aac aaa ctc aac acc    852
Leu Ala Val Met Gln Ala Tyr Asp Pro Glu Ile Asn Lys Leu Asn Thr
                210             215             220


atc ttg cag gag caa cgg atg gcc ttt aac att gct gag gct ttc aaa    900
Ile Leu Gln Glu Gln Arg Met Ala Phe Asn Ile Ala Glu Ala Phe Lys
225             230             235             240


gat gtg tca gaa ccc att gta ttt ctg caa cag atg cag gag ttt aga    948
Asp Val Ser Glu Pro Ile Val Phe Leu Gln Gln Met Gln Glu Phe Arg
                245             250             255
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　　　　　　　　　　　　　　　　　出証特２００２－３０３２９３５

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gag aaa atc aaa gta atc aag gaa act cct tta cct ccc tct aat ttg     996
Glu Lys Ile Lys Val Ile Lys Glu Thr Pro Leu Pro Pro Ser Asn Leu
            260             265             270


cct gca agc cct tta atg aag aac ttt gat acc agt cag tgg gaa gac    1044
Pro Ala Ser Pro Leu Met Lys Asn Phe Asp Thr Ser Gln Trp Glu Asp
            275             280             285


ata aaa cta gtc gat gtg gat aaa ctt tct ttg cct caa gac act ggc    1092
Ile Lys Leu Val Asp Val Asp Lys Leu Ser Leu Pro Gln Asp Thr Gly
            290             295             300


aca ttc att agc aag att ccc tgg agc ttt tat aag tta ttt ttg cta    1140
Thr Phe Ile Ser Lys Ile Pro Trp Ser Phe Tyr Lys Leu Phe Leu Leu
305             310             315             320


atc ctt ctg ctt ggc ctt gtc att gtc ttt ggt cct acc atg ttc cta    1188
Ile Leu Leu Leu Gly Leu Val Ile Val Phe Gly Pro Thr Met Phe Leu
            325             330             335


gaa tgg tca tta ttt gat gac ctg gca act tgg aaa ggc tgt ctt tca    1236
Glu Trp Ser Leu Phe Asp Asp Leu Ala Thr Trp Lys Gly Cys Leu Ser
            340             345             350


aac ttc agt tcc tat ctg act aaa aca gcc gat ttc ata gaa caa tca    1284
Asn Phe Ser Ser Tyr Leu Thr Lys Thr Ala Asp Phe Ile Glu Gln Ser
            355             360             365


gtt ttt tac tgg gaa cag gtg aca gat ggg ttt ttc att ttc aat gaa    1332
```

Val Phe Tyr Trp Glu Gln Val Thr Asp Gly Phe Phe Ile Phe Asn Glu
    370   375   380

aga ttc aag aat ttt act ttg gtg gta ctg aac aat gtg gca gaa ttt   1380
Arg Phe Lys Asn Phe Thr Leu Val Val Leu Asn Asn Val Ala Glu Phe
385   390   395   400

gtg tgc aaa tat aaa cta tta taaaatcg   1409
Val Cys Lys Tyr Lys Leu Leu
                405

<210> 97

<211> 465

<212> PRT

<213> Homo sapiens

<400> 97

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
 1   5   10   15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
                20   25   30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
                35   40   45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
    50   55   60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65   70   75   80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
              85   90   95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
            100   105   110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
            115   120   125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val
    130   135   140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145   150   155   160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
            165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
            180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
            195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn

```
           210                215                220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225                230                235                240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
                 245                250                255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
                 260                265                270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
                 275                280                285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu
                 290                295                300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305                310                315                320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
                 325                330                335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
                 340                345                350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
                 355                360                365
```

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
    370   375   380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385   390   395   400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
                405   410   415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
                420   425   430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
            435   440   445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
    450   455   460

Asp
465

<210> 98

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 98

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gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta  60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479
                                                                   Met
                                                                    1
```

```
gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
             5                  10                  15
```

```
atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
         20                  25                  30
```

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa   623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
    35   40   45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca   671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50   55   60   65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att   719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
            70   75   80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga   767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
            85   90   95

gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg   815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
    100   105   110

cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt   863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
    115   120   125

gaa gac gta tgc cag ggc tac aag gaa aag ctc cag gaa gct gtg aca   911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Glu Ala Val Thr
130   135   140   145

aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca   959

Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
             150   155   160

gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa   1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
             165   170   175

aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa   1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
             180   185   190

gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg   1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
             195   200   205

agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa   1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210   215   220   225

ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc   1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
             230   235   240

cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct   1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
             245   250   255

gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg   1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met

```
         260                    265                    270

tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt    1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
    275                    280                    285


cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta    1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290                    295                    300                    305


att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag    1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
                   310                    315                    320


aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg    1487
Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
                   325                    330                    335


ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt    1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
                   340                    345                    350


ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag    1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
    355                    360                    365


agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc    1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370                    375                    380                    385
```

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agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act     1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
            390                 395                 400


tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac     1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
            405                 410                 415


tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac     1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
            420                 425                 430


atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat     1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr
            435                 440                 445


ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac     1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450                 455                 460                 465


taaggaaaag agcagaagct ccttggttta accagcacag agaaataat ataaatccca 1931


taagggcag                                                          1940
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<210> 99

<211> 465

<212> PRT

<213> Homo sapiens

<400> 99

Met Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys
1   5   10   15

Ser Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly
                20   25   30

His Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser
                35   40   45

Gln Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala
                50   55   60

Pro Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu
65   70   75   80

Ile Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His
                85   90   95

Gly Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys
                100   105   110

Trp Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu
                115   120   125

Val Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val
                130   135   140

Thr Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser
145   150   155   160

Thr Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg
            165   170   175

Gln Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu
            180   185   190

Glu Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr
            195   200   205

Leu Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn
     210   215   220

Glu Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser
225   230   235   240

Ala Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp
            245   250   255

Ala Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr
            260   265   270

Met Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg
            275   280   285

Ser His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu

290   295   300

Leu Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln
305   310   315   320

Glu Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val
                       325   330   335

Leu Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp
                       340   345   350

Val Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val
                       355   360   365

Gln Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr
370   375   380

Leu Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro
385   390   395   400

Thr Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu
                       405   410   415

Asp Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys
                       420   425   430

His Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro
                       435   440   445

Tyr Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly
　　　450　　　　　　　　　455　　　　　　　　　460

Asp

465

<210> 100

<211> 1940

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (477)..(1871)

<400> 100

gttaacttcc tgacccagga agtggcagca acagagggga ctagcagcga atatacttta 60

caccaaatct cagaagattc agaacttaga tgagtggggc ccaggacagg aaccctggag 120

ccttggaagg aggggagccc catctcccca gaagagcagt gaccccagca gagaggggcc 180

tggtgtatca ctggaggaaa tagcctgcca aggaatacac gtcttcagaa gaagttctgt 240

gtggcttcaa gagactgatc aaattgtgag aggaaaacag cctacccggt cctcttttct 300

tcaatacaaa atgagataat aggggttgga aggaaaacct tcaagaccta tggaagtcag 360

ttgcagccag ctcatcacat agaggtgcag gtgaggtgta ttttcatcac ggtggaaaat 420

tctggctgct tcatctccat ctctagagcc aatattggag cttttcaata aaagct atg 479

                                                    Met

                                                    1

gcc tca acc acc agc acc aag aag atg atg gag gaa gcc acc tgc tcc   527
Ala Ser Thr Thr Ser Thr Lys Lys Met Met Glu Glu Ala Thr Cys Ser
            5   10   15

atc tgc ctg agc ctg atg acg aac cca gta agc atc aac tgt gga cac   575
Ile Cys Leu Ser Leu Met Thr Asn Pro Val Ser Ile Asn Cys Gly His
          20   25   30

agc tac tgc cac ttg tgt ata aca gac ttc ttt aaa aac cca agc caa   623
Ser Tyr Cys His Leu Cys Ile Thr Asp Phe Phe Lys Asn Pro Ser Gln
          35   40   45

aag caa ctg agg cag gag aca ttc tgc tgt ccc cag tgt cgg gct cca   671
Lys Gln Leu Arg Gln Glu Thr Phe Cys Cys Pro Gln Cys Arg Ala Pro
50   55   60   65

ttt cat atg gat agc ctc cga ccc aac aag cag ctg gga agc ctc att   719
Phe His Met Asp Ser Leu Arg Pro Asn Lys Gln Leu Gly Ser Leu Ile
          70   75   80

gaa gcc ctc aaa gag acg gat caa gaa atg tca tgt gag gaa cac gga   767
Glu Ala Leu Lys Glu Thr Asp Gln Glu Met Ser Cys Glu Glu His Gly
          85   90   95

```
gag cag ttc cac ctg ttc tgc gaa gac gag ggg cag ctc atc tgc tgg    815
Glu Gln Phe His Leu Phe Cys Glu Asp Glu Gly Gln Leu Ile Cys Trp
        100                 105                 110


cgc tgt gag cgg gca cca cag cac aaa ggg cac acc aca gct ctt gtt    863
Arg Cys Glu Arg Ala Pro Gln His Lys Gly His Thr Thr Ala Leu Val
        115                 120                 125


gaa gac gta tgc cag ggc tac aag gaa aag ctc cag aaa gct gtg aca    911
Glu Asp Val Cys Gln Gly Tyr Lys Glu Lys Leu Gln Lys Ala Val Thr
130                 135                 140                 145


aaa ctg aag caa ctt gaa gac aga tgt acg gag cag aag ctg tcc aca    959
Lys Leu Lys Gln Leu Glu Asp Arg Cys Thr Glu Gln Lys Leu Ser Thr
                150                 155                 160


gca atg cga ata act aaa tgg aaa gag aag gta cag att cag aga caa   1007
Ala Met Arg Ile Thr Lys Trp Lys Glu Lys Val Gln Ile Gln Arg Gln
            165                 170                 175


aaa atc cgg tct gac ttt aag aat ctc cag tgt ttc cta cat gag gaa   1055
Lys Ile Arg Ser Asp Phe Lys Asn Leu Gln Cys Phe Leu His Glu Glu
            180                 185                 190


gag aag tct tat ctc tgg agg ctg gag aaa gaa gaa caa cag act ctg   1103
Glu Lys Ser Tyr Leu Trp Arg Leu Glu Lys Glu Glu Gln Gln Thr Leu
            195                 200                 205
```

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agt aga ctg agg gac tat gag gct ggt ctg ggg ctg aag agc aat gaa    1151
Ser Arg Leu Arg Asp Tyr Glu Ala Gly Leu Gly Leu Lys Ser Asn Glu
210             215             220             225


ctc aag agc cac atc ctg gaa ctg gag gaa aaa tgt cag ggc tca gcc    1199
Leu Lys Ser His Ile Leu Glu Leu Glu Glu Lys Cys Gln Gly Ser Ala
                230             235             240


cag aaa ttg ctg cag aat gtg aat gac act ttg agc agg agt tgg gct    1247
Gln Lys Leu Leu Gln Asn Val Asn Asp Thr Leu Ser Arg Ser Trp Ala
                245             250             255


gtg aag ctg gaa aca tca gag gct gtc tcc ttg gaa ctt cat act atg    1295
Val Lys Leu Glu Thr Ser Glu Ala Val Ser Leu Glu Leu His Thr Met
                260             265             270


tgc aat gtt tcc aag ctt tac ttc gat gtg aag aaa atg tta agg agt    1343
Cys Asn Val Ser Lys Leu Tyr Phe Asp Val Lys Lys Met Leu Arg Ser
                275             280             285


cat caa gtt agt gtg act ctg gat cca gat aca gct cat cac gaa cta    1391
His Gln Val Ser Val Thr Leu Asp Pro Asp Thr Ala His His Glu Leu
290             295             300             305


att ctc tct gag gat cgg aga caa gtg act cgt gga tac acc cag gag    1439
Ile Leu Ser Glu Asp Arg Arg Gln Val Thr Arg Gly Tyr Thr Gln Glu
                310             315             320


aat cag gac aca tct tcc agg aga ttt act gcc ttc ccc tgt gtc ttg    1487
```

Asn Gln Asp Thr Ser Ser Arg Arg Phe Thr Ala Phe Pro Cys Val Leu
        325   330   335

ggt tgt gaa ggc ttc acc tca gga aga cgt tac ttt gaa gtg gat gtt   1535
Gly Cys Glu Gly Phe Thr Ser Gly Arg Arg Tyr Phe Glu Val Asp Val
        340   345   350

ggc gaa gga acc gga tgg gat tta gga gtt tgt atg gaa aat gtg cag   1583
Gly Glu Gly Thr Gly Trp Asp Leu Gly Val Cys Met Glu Asn Val Gln
        355   360   365

agg ggc act ggc atg aag caa gag cct cag tct gga ttc tgg acc ctc   1631
Arg Gly Thr Gly Met Lys Gln Glu Pro Gln Ser Gly Phe Trp Thr Leu
370   375   380   385

agg ctg tgc aaa aag aaa ggc tat gta gca ctt act tct ccc cca act   1679
Arg Leu Cys Lys Lys Lys Gly Tyr Val Ala Leu Thr Ser Pro Pro Thr
                 390   395   400

tcc ctt cat ctg cat gag cag ccc ctg ctt gtg gga att ttt ctg gac   1727
Ser Leu His Leu His Glu Gln Pro Leu Leu Val Gly Ile Phe Leu Asp
                 405   410   415

tat gag gcc gga gtt gta tcc ttt tat aac ggg aat act ggc tgc cac   1775
Tyr Glu Ala Gly Val Val Ser Phe Tyr Asn Gly Asn Thr Gly Cys His
                 420   425   430

atc ttt act ttc ccg aag gct tcc ttc tct gat act ctc cgg ccc tat   1823
Ile Phe Thr Phe Pro Lys Ala Ser Phe Ser Asp Thr Leu Arg Pro Tyr

```
          435                 440                 445


ttc cag gtt tat caa tat tct cct ttg ttt ctg cct ccc cca ggt gac   1871
Phe Gln Val Tyr Gln Tyr Ser Pro Leu Phe Leu Pro Pro Pro Gly Asp
450                 455                 460                 465


taaggaaaag agcagaagct ccttggttta accagcacag agaaaataat ataaatccca 1931


taagggcag                                                         1940
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<210> 101

<211> 685

<212> PRT

<213> Homo sapiens

<400> 101

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Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser Thr Lys
  1               5                  10                  15


Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser Lys Lys
                 20                  25                  30


Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln Ser Gln
                 35                  40                  45


Ala Gln Val Pro Pro Ala Ala Pro His His His His His His Ser His
          50                  55                  60
```

出証特２００２－３０３２９３５

Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr Gly Lys
65   70   75   80

Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala Lys Cys
                85   90   95

Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala Lys Ile
                100   105   110

Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys Ile Asp
                115   120   125

Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val Val Gln
                130   135   140

Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu Leu Glu
145   150   155   160

Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg Lys Val
                165   170   175

Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val Ser Gly
                180   185   190

Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu Lys Leu
                195   200   205

Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly Asp Phe
                210   215   220

Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg Thr Ile
225   230   235   240

Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys Gln Gly
               245   250   255

His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met Tyr Thr
               260   265   270

Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys Glu Thr
               275   280   285

Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser Leu Leu
               290   295   300

Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn Pro Glu
305   310   315   320

Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe Leu Gln
               325   330   335

Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr Val Pro
               340   345   350

Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys Ala Ala
               355   360   365

Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile Asp Thr

```
          370                  375                    380

His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu Arg His
385                  390                  395                  400

Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His Arg Thr
                 405                  410                  415

Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser Gly Thr
                 420                  425                  430

Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg Met Ile
             435                  440                  445

Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Glu Cys Leu Glu
             450                  455                  460

Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val Leu Arg
465                  470                  475                  480

Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys Glu Gln
                 485                  490                  495

Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr Ser Asn
                 500                  505                  510

Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly Val Leu
                 515                  520                  525
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Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys Thr Val
　530　　　　　　　 535　　　　　　　　 540

His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala Thr Asp
545　　　　　　　 550　　　　　　　 555　　　　　　　　 560

Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr Phe Ser
　　　　　　　 565　　　　　　　　 570　　　　　　　 575

His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro Ser Val
　　　　　　 580　　　　　　　　 585　　　　　　　 590

Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu Lys Ser
　　　　　　 595　　　　　　　 600　　　　　　　 605

Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln Val Asn
　610　　　　　　　 615　　　　　　　　 620

Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn Glu Glu
625　　　　　　　 630　　　　　　 635　　　　　　　　 640

Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr Phe Arg
　　　　　　　 645　　　　　　　 650　　　　　　　 655

Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys Asn Arg
　　　　　　 660　　　　　　　 665　　　　　　　 670

Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
　　　　　 675　　　　　　　 680　　　　　　　 685

<210> 102

<211> 2783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (128)..(2182)

<400> 102

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cggccggctc ggacgtgtga ccgcgcctag ggggtggcag cgggcagtgc ggggcggcaa  120

ggcgacc atg gag ctt ttg cgg act atc acc tac cag cca gcc gcc agc    169
        Met Glu Leu Leu Arg Thr Ile Thr Tyr Gln Pro Ala Ala Ser
        1                 5                   10

acc aaa atg tgc gag cag gcg ctg ggc aag ggt tgc gga gca gac tcg    217
Thr Lys Met Cys Glu Gln Ala Leu Gly Lys Gly Cys Gly Ala Asp Ser
15                  20                  25                  30

aag aag aag cgg ccg ccg cag ccc ccc gag gaa tcg cag cca cct cag    265
Lys Lys Lys Arg Pro Pro Gln Pro Pro Glu Glu Ser Gln Pro Pro Gln
                35                  40                  45

tcc cag gcg caa gtg ccc ccg gcg gcc cct cac cac cat cac cac cat    313
```

```
Ser Gln Ala Gln Val Pro Pro Ala Ala Pro His His His His His His
         50              55              60
```

```
tcg cac tcg ggg ccg gag atc tcg cgg att atc gtc gac ccc acg act   361
Ser His Ser Gly Pro Glu Ile Ser Arg Ile Ile Val Asp Pro Thr Thr
         65              70              75
```

```
ggg aag cgc tac tgc cgg ggc aaa gtg ctg gga aag ggt ggc ttt gca   409
Gly Lys Arg Tyr Cys Arg Gly Lys Val Leu Gly Lys Gly Gly Phe Ala
         80              85              90
```

```
aaa tgt tac gag atg aca gat ttg aca aat aac aaa gtc tac gcc gca   457
Lys Cys Tyr Glu Met Thr Asp Leu Thr Asn Asn Lys Val Tyr Ala Ala
 95              100             105             110
```

```
aaa att att cct cac agc aga gta gct aaa cct cat caa agg gaa aag   505
Lys Ile Ile Pro His Ser Arg Val Ala Lys Pro His Gln Arg Glu Lys
                 115             120             125
```

```
att gac aaa gaa ata gag ctt cac aga att ctt cat cat aag cat gta   553
Ile Asp Lys Glu Ile Glu Leu His Arg Ile Leu His His Lys His Val
         130             135             140
```

```
gtg cag ttt tac cac tac ttc gag gac aaa gaa aac att tac att ctc   601
Val Gln Phe Tyr His Tyr Phe Glu Asp Lys Glu Asn Ile Tyr Ile Leu
         145             150             155
```

```
ttg gaa tac tgc agt aga agg tca atg gct cat att ttg aaa gca aga   649
Leu Glu Tyr Cys Ser Arg Arg Ser Met Ala His Ile Leu Lys Ala Arg
```

160   165   170

```
aag gtg ttg aca gag cca gaa gtt cga tac tac ctc agg cag att gtg   697
Lys Val Leu Thr Glu Pro Glu Val Arg Tyr Tyr Leu Arg Gln Ile Val
175             180             185             190


tct gga ctg aaa tac ctt cat gaa caa gaa atc ttg cac aga gat ctc   745
Ser Gly Leu Lys Tyr Leu His Glu Gln Glu Ile Leu His Arg Asp Leu
            195             200             205


aaa cta ggg aac ttt ttt att aat gaa gcc atg gaa cta aaa gtt ggg   793
Lys Leu Gly Asn Phe Phe Ile Asn Glu Ala Met Glu Leu Lys Val Gly
            210             215             220


gac ttc ggt ctg gca gcc agg cta gaa ccc ttg gaa cac aga agg aga   841
Asp Phe Gly Leu Ala Ala Arg Leu Glu Pro Leu Glu His Arg Arg Arg
            225             230             235


acg ata tgt ggt acc cca aat tat ctc tct cct gaa gtc ctc aac aaa   889
Thr Ile Cys Gly Thr Pro Asn Tyr Leu Ser Pro Glu Val Leu Asn Lys
            240             245             250


caa gga cat ggc tgt gaa tca gac att tgg gcc ctg ggc tgt gta atg   937
Gln Gly His Gly Cys Glu Ser Asp Ile Trp Ala Leu Gly Cys Val Met
255             260             265             270


tat aca atg tta cta ggg agg ccc cca ttt gaa act aca aat ctc aaa   985
Tyr Thr Met Leu Leu Gly Arg Pro Pro Phe Glu Thr Thr Asn Leu Lys
            275             280             285
```

```
gaa act tat agg tgc ata agg gaa gca agg tat aca atg ccg tcc tca    1033
Glu Thr Tyr Arg Cys Ile Arg Glu Ala Arg Tyr Thr Met Pro Ser Ser
            290                 295                 300


ttg ctg gct cct gcc aag cac tta att gct agt atg ttg tcc aaa aac    1081
Leu Leu Ala Pro Ala Lys His Leu Ile Ala Ser Met Leu Ser Lys Asn
        305                 310                 315


cca gag gat cgt ccc agt ttg gat gac atc att cga cat gac ttt ttt    1129
Pro Glu Asp Arg Pro Ser Leu Asp Asp Ile Ile Arg His Asp Phe Phe
        320                 325                 330


ttg cag ggc ttc act ccg gac aga ctg tct tct agc tgt tgt cat aca    1177
Leu Gln Gly Phe Thr Pro Asp Arg Leu Ser Ser Ser Cys Cys His Thr
335                 340                 345                 350


gtt cca gat ttc cac tta tca agc cca gct aag aat ttc ttt aag aaa    1225
Val Pro Asp Phe His Leu Ser Ser Pro Ala Lys Asn Phe Phe Lys Lys
                355                 360                 365


gca gct gct gct ctt ttt ggt ggc aaa aaa gac aaa gca aga tat att    1273
Ala Ala Ala Ala Leu Phe Gly Gly Lys Lys Asp Lys Ala Arg Tyr Ile
            370                 375                 380


gac aca cat aat aga gtg tct aaa gaa gat gaa gac atc tac aag ctt    1321
Asp Thr His Asn Arg Val Ser Lys Glu Asp Glu Asp Ile Tyr Lys Leu
            385                 390                 395
```

agg cat gat ttg aaa aag act tca ata act cag caa ccc agc aaa cac   1369
Arg His Asp Leu Lys Lys Thr Ser Ile Thr Gln Gln Pro Ser Lys His
    400   405   410

agg aca gat gag gag ctc cag cca cct acc acc aca gtt gcc agg tct   1417
Arg Thr Asp Glu Glu Leu Gln Pro Pro Thr Thr Thr Val Ala Arg Ser
415   420   425   430

gga aca ccc gca gta gaa aac aag cag cag att ggg gat gct att cgg   1465
Gly Thr Pro Ala Val Glu Asn Lys Gln Gln Ile Gly Asp Ala Ile Arg
                435   440   445

atg ata gtc aga ggg act ctt ggc agc tgt agc agc agc agt gaa tgc   1513
Met Ile Val Arg Gly Thr Leu Gly Ser Cys Ser Ser Ser Ser Glu Cys
                450   455   460

ctt gaa gac agt acc atg gga agt gtt gca gac aca gtg gca agg gtt   1561
Leu Glu Asp Ser Thr Met Gly Ser Val Ala Asp Thr Val Ala Arg Val
                465   470   475

ctt cgg gga tgt ctg gaa aac atg ccg gaa gct gat tgc att ccc aaa   1609
Leu Arg Gly Cys Leu Glu Asn Met Pro Glu Ala Asp Cys Ile Pro Lys
    480   485   490

gag cag ctg agc aca tca ttt cag tgg gtc acc aaa tgg gtt gat tac   1657
Glu Gln Leu Ser Thr Ser Phe Gln Trp Val Thr Lys Trp Val Asp Tyr
495   500   505   510

tct aac aaa tat ggc ttt ggg tac cag ctc tca gac cac acc gtc ggt   1705

```
Ser Asn Lys Tyr Gly Phe Gly Tyr Gln Leu Ser Asp His Thr Val Gly
            515                 520                 525
```

```
gtc ctt ttc aac aat ggt gct cac atg agc ctc ctt cca gac aaa aaa     1753
Val Leu Phe Asn Asn Gly Ala His Met Ser Leu Leu Pro Asp Lys Lys
            530                 535                 540
```

```
aca gtt cac tat tac gca gag ctt ggc caa tgc tca gtt ttc cca gca     1801
Thr Val His Tyr Tyr Ala Glu Leu Gly Gln Cys Ser Val Phe Pro Ala
            545                 550                 555
```

```
aca gat gct cct gag caa ttt att agt caa gtg acg gtg ctg aaa tac     1849
Thr Asp Ala Pro Glu Gln Phe Ile Ser Gln Val Thr Val Leu Lys Tyr
        560                 565                 570
```

```
ttt tct cat tac atg gag gag aac ctc atg gat ggt gga gat ctg cct     1897
Phe Ser His Tyr Met Glu Glu Asn Leu Met Asp Gly Gly Asp Leu Pro
575                 580                 585                 590
```

```
agt gtt act gat att cga aga cct cgg ctc tac ctc ctt cag tgg cta     1945
Ser Val Thr Asp Ile Arg Arg Pro Arg Leu Tyr Leu Leu Gln Trp Leu
            595                 600                 605
```

```
aaa tct gat aag gcc cta atg atg ctc ttt aat gat ggc acc ttt cag     1993
Lys Ser Asp Lys Ala Leu Met Met Leu Phe Asn Asp Gly Thr Phe Gln
            610                 615                 620
```

```
gtg aat ttc tac cat gat cat aca aaa atc atc atc tgt agc caa aat     2041
Val Asn Phe Tyr His Asp His Thr Lys Ile Ile Ile Cys Ser Gln Asn
```

```
                625                    630                    635


gaa gaa tac ctt ctc acc tac atc aat gag gat agg ata tct aca act    2089
Glu Glu Tyr Leu Leu Thr Tyr Ile Asn Glu Asp Arg Ile Ser Thr Thr
        640                    645                    650


ttc agg ctg aca act ctg ctg atg tct ggc tgt tca tca gaa tta aaa    2137
Phe Arg Leu Thr Thr Leu Leu Met Ser Gly Cys Ser Ser Glu Leu Lys
655                    660                    665                    670


aat cga atg gaa tat gcc ctg aac atg ctc tta caa aga tgt aac        2182
Asn Arg Met Glu Tyr Ala Leu Asn Met Leu Leu Gln Arg Cys Asn
            675                    680                    685


tgaaagactt ttcgaatgga ccctatggga ctcctctttt ccactgtgag atctacaggg 2242


aacccaaaag aatgatctag agtatgttga agaagatgga catgtggtgg tacgaaaaca 2302


attcccctgt ggcctgctgg actgggtgga accagaacag gctaaggcat acagttcttg 2362


actttggaca atccaagagt gaaccagaat gcagttttcc ttgagatacc tgttttaaaa 2422


ggttttttcag acaattttgc agaaaggtgc attgattctt aaattctctc tgttgagagc 2482


atttcagcca gaggactttg gaactgtgaa tatacttcct gaaggggagg gagaagggag 2542


gaagctccca tgttgtttaa aggctgtaat tggagcagct tttggctgcg taactgtgaa 2602


ctatggccat atataatttt ttttcattaa ttttttgaaga tacttgtggc tggaaaagtg 2662
```

cattccttgt aataaactt tttatttatt acagcccaaa gagcagtatt tattatcaaa 2722

atgtctttt ttttatgttg accattttaa accgttggca ataaagagta tgaaaacgca 2782

g   2783

<210> 103

<211> 161

<212> PRT

<213> Homo sapiens

<400> 103

```
Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1               5                   10                  15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
            20                  25                  30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
            35                  40                  45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
    50                  55                  60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
    65                  70                  75                  80
```

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met Cys Cys
               85   90   95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
        100   105   110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
        115   120   125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
        130   135   140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145   150   155   160

Leu

<210> 104

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 104

cctttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc 111
          Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
          1   5   10

tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac   159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15   20   25   30

agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg   207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
                35   40   45

ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat   255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
                50   55   60

acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg   303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
          65   70   75

gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct atc caa atg   351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Ile Gln Met
  80   85   90

tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac   399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
 95   100   105   110

```
gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg      447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
             115                 120                 125


tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag      495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
             130                 135                 140


gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac      543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
             145                 150                 155


aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg              592
Lys Arg Leu
      160


aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc    652


acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac    712


aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc    772


cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa    832


ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctctttttc    892


ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt    952
```

```
ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg ctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt cttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

tgggcctgaa cataatttca agaggaggat ttataaaacc attttctgta atcaaatgat 1552

tggtgtcatt ttcccatttg ccaatgtagt ctcactt                         1589
```

<210> 105

<211> 161

<212> PRT

<213> Homo sapiens

<400> 105

Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser Ser Ala
1   5   10   15

Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn Ser Tyr
            20   25   30

Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly Leu Val
            35   40   45

Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr Thr Gln
            50   55   60

Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr Val Tyr
65   70   75   80

Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met Cys Cys
                    85   90   95

Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn Ala Gly
                    100   105   110

Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly Cys Ile
            115   120   125

Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln Asp Val
            130   135   140

Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr Lys Arg
145   150   155   160

Leu

<210> 106

<211> 1589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(552)

<400> 106

cctttctcg gggcgcccga aggccagctc agacctcccg gctcgacagg cggcgcgggc 60

```
ggcggtaaa atg tcg gtt cca gga cct tac cag gcg gcc act ggg cct tcc  111
           Met Ser Val Pro Gly Pro Tyr Gln Ala Ala Thr Gly Pro Ser
            1               5                  10
```

```
tca gca cca tcc gca cct cca tcc tat gaa gag aca gtg gct gtt aac   159
Ser Ala Pro Ser Ala Pro Pro Ser Tyr Glu Glu Thr Val Ala Val Asn
 15                 20                 25                 30
```

```
agt tat tac ccc aca cct cca gct ccc atg cct ggg cca act acg ggg   207
Ser Tyr Tyr Pro Thr Pro Pro Ala Pro Met Pro Gly Pro Thr Thr Gly
                35                 40                 45
```

```
ctt gtg acg ggg cct gat ggg aag ggc atg aat cct cct tcg tat tat          255
Leu Val Thr Gly Pro Asp Gly Lys Gly Met Asn Pro Pro Ser Tyr Tyr
            50                  55                  60


acc cag cca gcg ccc atc ccc aat aac aat cca att acc gtg cag acg          303
Thr Gln Pro Ala Pro Ile Pro Asn Asn Asn Pro Ile Thr Val Gln Thr
            65                  70                  75


gtc tac gtg cag cac ccc atc acc ttt ttg gac cgc cct gtc caa atg          351
Val Tyr Val Gln His Pro Ile Thr Phe Leu Asp Arg Pro Val Gln Met
            80                  85                  90


tgt tgt cct tcc tgc aac aag atg atc gtg agt cag ctg tcc tat aac          399
Cys Cys Pro Ser Cys Asn Lys Met Ile Val Ser Gln Leu Ser Tyr Asn
    95                  100                 105                 110


gcc ggt gct ctg acc tgg ctg tcc tgc ggg agc ctg tgc ctg ctg ggg          447
Ala Gly Ala Leu Thr Trp Leu Ser Cys Gly Ser Leu Cys Leu Leu Gly
                115                 120                 125


tgc ata gcg ggc tgc tgc ttc atc ccc ttc tgc gtg gat gcc ctg cag          495
Cys Ile Ala Gly Cys Cys Phe Ile Pro Phe Cys Val Asp Ala Leu Gln
                130                 135                 140


gac gtg gac cat tac tgt ccc aac tgc aga gct ctc ctg ggc acc tac          543
Asp Val Asp His Tyr Cys Pro Asn Cys Arg Ala Leu Leu Gly Thr Tyr
                145                 150                 155


aag cgt ttg taggactcag ccagacgtgg agggagccgg gtgccgcagg                   592
Lys Arg Leu
```

Lys Arg Leu

160

aagtcctttc cacctctcat ccagcttcac gcctggtgga ggttctgccc tggtggtctc 652

acctctccag ggggcccacc ttcatgtctt cttttggggg gaatacgtcg caaaactaac 712

aaatctccaa accccagaaa ttgctgcttg gagtcgtgca taggacttgc aaagacattc 772

cccttgagtg tcagttccac ggtttcctgc ctccctgaga ccctgagtcc tgccatctaa 832

ctgtgatcat tgccctatcc gaatatcttc ctgtgatctg ccatcagtgg ctcttttttc 892

ctgcttccat gggcctttct ggtggcagtc tcaaactgag aagccacagt tgccttattt 952

ttgaggctgt tctgcccaga gctcggctga accagccttt agtgcctacc attatcttat 1012

ccgtctcttc ccgtccctga tgacaaagat cttgccttac agactttaca ggcttggctt 1072

tgagattctg taactgcaga cttcattagc acacagattc actttaattt cttaattttt 1132

tttttaaata caaggagggg gctattaaca cccagtacag acatatccac aaggtcgtaa 1192

atgcatgcta gaaaaatagg gctggatctt atcactgccc tgtctcccct tgtttctctg 1252

tgccagatct tcagtgcccc tttccataca gggatttttt tctcatagag taattatatg 1312

aacagttttt atgacctcct tttggtctga aatactttcg aacagaattt ctttttttta 1372

aaaaaaaaca gagatggggt cttactatgt tgcccaggct ggtgtcgaac tcctgggctc 1432

aagcgatcct tctgccttgg cctcccgaag tgctgggatt gcaggcataa gctaccatgc 1492

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tggtgtcatt ttcccatttg ccaatgtagt ctcactt 1589

<210> 107

<211> 249

<212> PRT

<213> Homo sapiens

<400> 107

Met Ala Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val
1   5   10   15

Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val
                20   25   30

Val Thr Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys
            35   40   45

Phe Lys Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn
        50   55   60

Ser Gly Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu
65   70   75   80

Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met
           85   90   95

Val Gln Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val
         100   105   110

Trp Lys Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys
         115   120   125

Val Phe Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro
         130   135   140

Ser Lys Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro
145   150   155   160

Lys Pro His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met
         165   170   175

Glu Glu Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu
         180   185   190

Asn Arg His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His
         195   200   205

Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val
         210   215   220

Thr Ser Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile

225   230   235   `240

Gly Phe Phe Leu Gly Lys Phe Ile Leu
                  245

<210> 108

<211> 1595

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(978)

<400> 108

agtgcgcgtg gccgtggcgg ctggtgtggg gttgagtcag ttgtgggacc cggagctgct 60

gacccagcgg gtggcccacc gaaccggtga cacagcggca ggcgttaggg ctcgggagcc 120

gcgagcctgg cctcgtccta gagctcggcc gagccgtcgc cgccgtcgtc ccccgccccc 180

agtcagcaaa ccgccgccgc gggcgcgccc ccgctctgcg ctgtctctcc g atg gcg 237
                                                          Met Ala
                                                           1

tcc gcc tca ggg gcc atg gcg aag cac gag cag atc ctg gtc ctc gat 285
Ser Ala Ser Gly Ala Met Ala Lys His Glu Gln Ile Leu Val Leu Asp
        5   10   15

```
ccg ccc aca gac ctc aaa ttc aaa ggc ccc ttc aca gat gta gtc act    333
Pro Pro Thr Asp Leu Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr
    20                  25                  30


aca aat ctt aaa ttg cga aat cca tcg gat aga aaa gtg tgt ttc aaa    381
Thr Asn Leu Lys Leu Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys
    35                  40                  45                  50


gtg aag act aca gca cct cgc cgg tac tgt gtg agg ccc aac agt gga    429
Val Lys Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly
                55                  60                  65


att att gac cca ggg tca act gtg act gtt tca gta atg cta cag ccc    477
Ile Ile Asp Pro Gly Ser Thr Val Thr Val Ser Val Met Leu Gln Pro
                70                  75                  80


ttt gac tat gat ccg aat gaa aag agt aaa cac aag ttt atg gta cag    525
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val Gln
                85                  90                  95


aca att ttt gct cca cca aac act tca gat atg gaa gct gtg tgg aaa    573
Thr Ile Phe Ala Pro Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys
    100                 105                 110


gag gca aaa cct gat gaa tta atg gat tcc aaa ttg aga tgc gta ttt    621
Glu Ala Lys Pro Asp Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe
    115                 120                 125                 130
```

```
gaa atg ccc aat gaa aat gat aaa ttg aat gat atg gaa cct agc aaa      669
Glu Met Pro Asn Glu Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys
                135             140             145


gct gtt cca ctg aat gca tct aag caa gat gga cct atg cca aaa cca      717
Ala Val Pro Leu Asn Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro
                150             155             160


cac agt gtt tca ctt aat gat acc gaa aca agg aaa cta atg gaa gag      765
His Ser Val Ser Leu Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu
                165             170             175


tgt aaa aga ctt cag gga gaa atg atg aag cta tca gaa gaa aat cgg      813
Cys Lys Arg Leu Gln Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg
                180             185             190


cac ctg aga gat gaa ggt tta agg ctc aga aag gta gca cat tcg gat      861
His Leu Arg Asp Glu Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp
195             200             205             210


aaa cct gga tca acc tca act gca tcc ttc aga gat aat gtc acc agt      909
Lys Pro Gly Ser Thr Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser
                215             220             225


cct ctt cct tca ctt ctt gtt gta att gca gcc att ttc att gga ttc      957
Pro Leu Pro Ser Leu Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe
                230             235             240


ttt cta ggg aaa ttc atc ttg tagagtgaag catgcagagt gctgtttctt        1008
Phe Leu Gly Lys Phe Ile Leu
```

Phe Leu Gly Lys Phe Ile Leu

      245

tttttttttt tctcttgacc agaaaaagat ttgtttacct accatttcat tggtagtatg 1068

gcccacggtg accatttttt tgtgtgtaca gcgtcatata ggctttgcct ttaatgatct 1128

cttacggtta gaaaacacaa taaaaacaaa ctgttcggct actggacagg ttgtatatta 1188

ccagatcatc actagcagat gtcagttgca cattgagtcc tttatgaaat tcataaataa 1248

agaattgttc tttctttgtg gttttaataa gagttcaaga attgttcaga gtcttgtaaa 1308

tgttatttta ataatccctt taaattttat ctgttgctgt tacctcttga aatatgattt 1368

atttagattg ctaatcccac tcattcagga aatgccaaga ggtattcctt ggggaaatgg 1428

tgcctcttac agtgtaaatt tttcctcctt tacctttgct aatatcatgg cagaattttt 1488

cttatccctt gtgaggcagt tgttgactga gtttttcatc cttacaatcc tgtcccatgg 1548

tatttaacat aaaaaaaaat aaaactgtta acagattctt gctcgat   1595

<210> 109

<211> 540

<212> PRT

<213> Homo sapiens

<400> 109

```
Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
1               5                   10                  15


Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
                20                  25                  30


Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
            35                  40                  45


Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
            50                  55                  60


His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65                  70                  75                  80


Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85                  90                  95


Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
                100                 105                 110


Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
                115                 120                 125


Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser
                130                 135                 140


Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
```

```
        145                    150                    155                    160
```

Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
```
             165                    170                    175
```

Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
```
             180                    185                    190
```

Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
```
             195                    200                    205
```

Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
```
        210                    215                    220
```

Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
```
   225                    230                    235                    240
```

Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
```
             245                    250                    255
```

Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
```
             260                    265                    270
```

Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
```
             275                    280                    285
```

Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
```
             290                    295                    300
```

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305   310   315   320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
        325   330   335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
        340   345   350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
        355   360   365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
        370   375   380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385   390   395   400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg
            405   410   415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
        420   425   430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
        435   440   445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
        450   455   460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465   470   475   480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
            485   490   495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
            500   505   510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
            515   520   525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
            530   535   540

<210> 110

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 110

aaccgtaaca gccaccagac aagcttcagt ggccggcccт tcacatccag acttgcctga 60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc 116
　　　　　　　　　　　　　　　　　　　　　　　　　Met Gly Thr Thr Ala
　　　　　　　　　　　　　　　　　　　　　　　　　1　　　　　　　5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 　164
Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
　　　　　　　　10　　　　　　　　15　　　　　　　　20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 　212
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
　　　　　　　　25　　　　　　　　30　　　　　　　　35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 　260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
　　　　　　　　40　　　　　　　　45　　　　　　　　50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 　308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
　　　　　　　　55　　　　　　　　60　　　　　　　　65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 　356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70　　　　　　　　75　　　　　　　　80　　　　　　　　85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 　404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu
　　　　　　　　90　　　　　　　　95　　　　　　　　100

gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg 　452

```
Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
        105             110             115
```

```
ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca    500
Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
        120             125             130
```

```
ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag    548
Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
        135             140             145
```

```
cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat    596
His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
150             155             160             165
```

```
ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc    644
Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
            170             175             180
```

```
ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag    692
Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
            185             190             195
```

```
tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg    740
Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
        200             205             210
```

```
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc    788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
```

```
        215                  220                  225


cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt    836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230                  235                  240                  245


gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg    884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
                    250                  255                  260


cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca    932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
                    265                  270                  275


cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg    980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
                    280                  285                  290


ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc   1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
                    295                  300                  305


aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg   1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310                  315                  320                  325


cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg   1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
                    330                  335                  340
```

```
gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt   1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
            345                 350                 355


aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag   1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
            360                 365                 370


tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc   1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
            375                 380                 385


cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat   1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390                 395                 400                 405


gac cgg gac atc ttg acc att gac atc ggt cga gtc acc ccc aac ctc   1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Gly Arg Val Thr Pro Asn Leu
                410                 415                 420


atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat   1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
            425                 430                 435


att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca   1460
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
            440                 445                 450
```

```
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc      1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
    455             460             465


aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc      1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
470             475             480             485


tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc      1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
            490             495             500


aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc      1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
        505             510             515


aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc      1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
        520             525             530


acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga         1751
Thr Ser Glu Pro Lys Glu Glu
        535             540



tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg    1810
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<210> 111

<211> 540

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Thr Thr Ala Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val
1   5   10   15

Ala Ser Ala Ala Ser Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln
                20   25   30

Leu Arg Pro Glu His Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser
        35   40   45

Pro Pro Leu Ser Arg Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln
        50   55   60

His Gly Pro Pro Phe Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser
65   70   75   80

Gln Glu Ala Thr Pro Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu
                85   90   95

Pro Ala Glu Lys Glu Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro
                100   105   110

Leu Gln Lys Glu Leu Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu
            115   120   125

Gly Thr Pro Ala Pro Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser

```
              130                    135                        140


Trp Asn Ala Ala Gln His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp
145                   150                155                160


Gly His Arg Leu Asp Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn
                  165                170                175


Leu Asn Gln Ile Cys Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro
                  180                185                190


Trp Asn Leu Pro Gln Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu
                  195                200                205


Thr Leu Asn Phe Leu Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg
210                   215                220


Ser His Thr Asn Arg Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala
225                   230                235                240


Met Ser Arg Phe Cys Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His
                  245                250                255


Trp Cys Cys Thr Arg Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu
                  260                265                270


Glu Ala Pro Gln Pro His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln
                  275                280                285
```

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Pro Asp Ile Ser Ser Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro
    290   295   300

Thr Leu Asp Asn Ile Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser
305   310   315   320

Val Pro Arg Asn Leu Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu
                325   330   335

Ala Leu Ile Gln Leu Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly
                340   345   350

Asn Asn His Thr Cys Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys
                355   360   365

Tyr Cys Asp Arg Glu Tyr Ala Val Lys Thr His His His Leu Cys Cys
370   375   380

Arg His Pro Pro Ser Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala
385   390   395   400

Pro Tyr Pro Asn Tyr Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg
                405   410   415

Val Thr Pro Asn Leu Met Gly His Leu Cys Gly Asn Gln Arg Val Leu
                420   425   430

Thr Lys His Lys His Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg
                435   440   445

Cys Cys Asp Leu Pro Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu
　　450　　　　　　　　455　　　　　　　　460

Lys Leu Thr Phe Ile Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp
465　　　　　　　　470　　　　　　　　475　　　　　　　　480

Arg Asp Pro Ala Leu Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val
　　　　485　　　　　　　　490　　　　　　　　495

Asn Cys Phe Asn Ile Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly
　　500　　　　　　　　505　　　　　　　　510

Asp Thr Glu Asn Ala Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly
　　515　　　　　　　　520　　　　　　　　525

Thr Asn Ile Ser Ser Thr Ser Glu Pro Lys Glu Glu
　　530　　　　　　　　535　　　　　　　　540

<210> 112

<211> 1810

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)..(1721)

<400> 112

aaccgtaaca gccaccagac aagcttcagt ggccggccct tcacatccag acttgcctga 60

gaggacccac ctctgagtgt ccagtggtca gttgccccag g atg ggg acc aca gcc 116
                                              Met Gly Thr Thr Ala
                                              1   5

aga gca gcc ttg gtc ttg acc tat ttg gct gtt gct tct gct gcc tct 164
Arg Ala Ala Leu Val Leu Thr Tyr Leu Ala Val Ala Ser Ala Ala Ser
            10   15   20

gag gga ggc ttc acg gct aca gga cag agg cag ctg agg cca gag cac 212
Glu Gly Gly Phe Thr Ala Thr Gly Gln Arg Gln Leu Arg Pro Glu His
            25   30   35

ttt caa gaa gtt ggc tac gca gct ccc ccc tcc cca ccc cta tcc cga 260
Phe Gln Glu Val Gly Tyr Ala Ala Pro Pro Ser Pro Pro Leu Ser Arg
            40   45   50

agc ctc ccc atg gat cac cct gac tcc tct cag cat ggc cct ccc ttt 308
Ser Leu Pro Met Asp His Pro Asp Ser Ser Gln His Gly Pro Pro Phe
            55   60   65

gag gga cag agt caa gtg cag ccc cct ccc tct cag gag gcc acc cct 356
Glu Gly Gln Ser Gln Val Gln Pro Pro Pro Ser Gln Glu Ala Thr Pro
70   75   80   85

ctc caa cag gaa aag ctg cta cct gcc caa ctc cct gct gaa aag gaa 404
Leu Gln Gln Glu Lys Leu Leu Pro Ala Gln Leu Pro Ala Glu Lys Glu

```
                    90                      95                     100


        gtg ggt ccc cct ctc cct cag gaa gct gtc ccc ctc caa aaa gag ctg    452
        Val Gly Pro Pro Leu Pro Gln Glu Ala Val Pro Leu Gln Lys Glu Leu
                    105                     110                    115


        ccc tct ctc cag cac ccc aat gaa cag aag gaa gga acg cca gct cca    500
        Pro Ser Leu Gln His Pro Asn Glu Gln Lys Glu Gly Thr Pro Ala Pro
                    120                     125                    130


        ttt ggg gac cag agc cat cca gaa cct gag tcc tgg aat gca gcc cag    548
        Phe Gly Asp Gln Ser His Pro Glu Pro Glu Ser Trp Asn Ala Ala Gln
                  135                     140                    145


        cac tgc caa cag gac cgg tcc caa ggg ggc tgg ggc cac cgg ctg gat    596
        His Cys Gln Gln Asp Arg Ser Gln Gly Gly Trp Gly His Arg Leu Asp
        150                     155                     160                    165


        ggc ttc ccc cct ggg cgg cct tct cca gac aat ctg aac caa atc tgc    644
        Gly Phe Pro Pro Gly Arg Pro Ser Pro Asp Asn Leu Asn Gln Ile Cys
                    170                     175                    180


        ctt cct aac cgt cag cat gtg gta tat ggt ccc tgg aac cta cca cag    692
        Leu Pro Asn Arg Gln His Val Val Tyr Gly Pro Trp Asn Leu Pro Gln
                    185                     190                    195


        tcc agc tac tcc cac ctc act cgc cag ggt gag acc ctc aat ttc ctg    740
        Ser Ser Tyr Ser His Leu Thr Arg Gln Gly Glu Thr Leu Asn Phe Leu
                    200                     205                    210
```

```
gag att gga tat tcc cgc tgc tgc cac tgc cgc agc cac aca aac cgc     788
Glu Ile Gly Tyr Ser Arg Cys Cys His Cys Arg Ser His Thr Asn Arg
    215             220             225


cta gag tgt gcc aaa ctt gtg tgg gag gaa gca atg agc cga ttc tgt     836
Leu Glu Cys Ala Lys Leu Val Trp Glu Glu Ala Met Ser Arg Phe Cys
230             235             240             245


gag gcc gag ttc tcg gtc aag acc cga ccc cac tgg tgc tgc acg cgg     884
Glu Ala Glu Phe Ser Val Lys Thr Arg Pro His Trp Cys Cys Thr Arg
        250             255             260


cag ggg gag gct cgg ttc tcc tgc ttc cag gag gaa gct ccc cag cca     932
Gln Gly Glu Ala Arg Phe Ser Cys Phe Gln Glu Glu Ala Pro Gln Pro
        265             270             275


cac tac cag ctc cgg gcc tgc ccc agc cat cag cct gat att tcc tcg     980
His Tyr Gln Leu Arg Ala Cys Pro Ser His Gln Pro Asp Ile Ser Ser
        280             285             290


ggt ctt gag ctg cct ttc cct cct ggg gtg ccc aca ttg gac aat atc    1028
Gly Leu Glu Leu Pro Phe Pro Pro Gly Val Pro Thr Leu Asp Asn Ile
        295             300             305


aag aac atc tgc cac ctg agg cgc ttc cgc tct gtg cca cgc aac ctg    1076
Lys Asn Ile Cys His Leu Arg Arg Phe Arg Ser Val Pro Arg Asn Leu
310             315             320             325
```

```
cca gct act gac ccc cta caa agg gag ctg ctg gca ctg atc cag ctg      1124
Pro Ala Thr Asp Pro Leu Gln Arg Glu Leu Leu Ala Leu Ile Gln Leu
                330             335                 340


gag agg gag ttc cag cgc tgc tgc cgc cag ggg aac aat cac acc tgt      1172
Glu Arg Glu Phe Gln Arg Cys Cys Arg Gln Gly Asn Asn His Thr Cys
                345             350                 355


aca tgg aag gcc tgg gag gat acc ctt gac aaa tac tgt gac cgg gag      1220
Thr Trp Lys Ala Trp Glu Asp Thr Leu Asp Lys Tyr Cys Asp Arg Glu
                360             365                 370


tat gct gtg aag acc cac cac cac ttg tgt tgc cgc cac cct ccc agc      1268
Tyr Ala Val Lys Thr His His His Leu Cys Cys Arg His Pro Pro Ser
                375             380                 385


cct act cgg gat gag tgc ttt gcc cgt cgg gct cct tac ccc aac tat      1316
Pro Thr Arg Asp Glu Cys Phe Ala Arg Arg Ala Pro Tyr Pro Asn Tyr
390             395                 400                 405


gac cgg gac atc ttg acc att gac atc agt cga gtc acc ccc aac ctc      1364
Asp Arg Asp Ile Leu Thr Ile Asp Ile Ser Arg Val Thr Pro Asn Leu
                410             415                 420


atg ggc cac ctc tgt gga aac caa aga gtt ctc acc aag cat aaa cat      1412
Met Gly His Leu Cys Gly Asn Gln Arg Val Leu Thr Lys His Lys His
                425             430                 435


att cct ggg ctg atc cac aac atg act gcc cgc tgc tgt gac ctg cca      1460
```

```
Ile Pro Gly Leu Ile His Asn Met Thr Ala Arg Cys Cys Asp Leu Pro
    440                 445             450
```

```
ttt cca gaa cag gcc tgc tgt gca gag gag gag aaa tta acc ttc atc    1508
Phe Pro Glu Gln Ala Cys Cys Ala Glu Glu Glu Lys Leu Thr Phe Ile
    455             460             465
```

```
aat gat ctg tgt ggt ccc cga cgt aac atc tgg cga gac cct gcc ctc    1556
Asn Asp Leu Cys Gly Pro Arg Arg Asn Ile Trp Arg Asp Pro Ala Leu
470             475             480             485
```

```
tgc tgt tac ctg agt cct ggg gat gaa cag gtc aac tgc ttc aac atc    1604
Cys Cys Tyr Leu Ser Pro Gly Asp Glu Gln Val Asn Cys Phe Asn Ile
                490             495             500
```

```
aat tat ctg agg aac gtg gct cta gtg tct gga gac act gag aac gcc    1652
Asn Tyr Leu Arg Asn Val Ala Leu Val Ser Gly Asp Thr Glu Asn Ala
            505             510             515
```

```
aag ggc cag ggg gag cag ggc tca act gga gga aca aat atc agc tcc    1700
Lys Gly Gln Gly Glu Gln Gly Ser Thr Gly Gly Thr Asn Ile Ser Ser
    520             525             530
```

```
acc tct gag ccc aag gaa gaa tgagtcaccc cagagcccta gagggtcaga    1751
Thr Ser Glu Pro Lys Glu Glu
    535             540
```

```
tggggggaac cccaccctgc cccacccatc tgaacactca ttacactaaa cacctcttg    1810
```

<210> 113

<211> 382

<212> PRT

<213> Homo sapiens

<400> 113

Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
1   5   10   15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
            20   25   30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
        35   40   45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
        50   55   60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
65   70   75   80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
                85   90   95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
                100   105   110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys

```
        115                  120                  125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
        130                  135                  140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145                  150                  155                  160

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
                165                  170                  175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
                180                  185                  190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
                195                  200                  205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
        210                  215                  220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225                  230                  235                  240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
                245                  250                  255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
                260                  265                  270
```

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
        275   280   285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
        290   295   300

Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
305   310   315   320

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
                325   330   335

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
                340   345   350

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
                355   360   365

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
        370   375   380

<210> 114

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 114

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aacagcagcg gagttttaaa ctttaaatag acaggtctga gtgcctgaac ttgccttttc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
　　　　　　　　　　　　　　Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
　　　　　　　　　　　　　　　1　　　　　　　　　5　　　　　　　　　　　10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca　281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
　　　　　　　15　　　　　　　　　　20　　　　　　　　　　25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca　329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
　　　30　　　　　　　　　　35　　　　　　　　　　40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct　377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
　　　45　　　　　　　　　　50　　　　　　　　　　55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg　425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
　　60　　　　　　　　　　65　　　　　　　　　　70　　　　　　　　　　75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg   473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
               80   85   90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac   521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
               95   100   105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg   569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
       110   115   120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att   617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
       125   130   135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac   665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140   145   150   155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg   713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
              160   165   170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc   761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
              175   180   185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc   809

```
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
        190             195             200
```

```
acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg   857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
        205             210             215
```

```
tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc   905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
 220             225             230             235
```

```
gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt   953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
            240             245             250
```

```
ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat  1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
            255             260             265
```

```
ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct  1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
            270             275             280
```

```
cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc  1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
            285             290             295
```

```
aat tac aac aag caa gca agt gag caa acc tgg gct aat tac agt gca  1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Thr Trp Ala Asn Tyr Ser Ala
```

```
      300                  305                  310                  315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat   1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
                  320              . 325                  330


gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta   1241
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
              335                  340                  345


gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct   1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
          350                  355                  360


tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac   1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
      365                  370                  375


ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt          1386
Leu Glu Ile
380


ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446


ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506


tcactggggg tgtatggggt agatgggtgg agagggaggg dataagagag gtgcatgttg 1566


gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
```

catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686

gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746

ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806

gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc actttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt tttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgttaattat gattctttat tttctctcct tttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtcttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

agaggattca gtagtacaca tacaactaat ttatttgaac tatatgttga agacatctac 2826

cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

tgacactttt cttcttgcat gcatgtcagc tacataaaca gttttgtaca atgaaaatta 2946

ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

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tttagtat   3074

<210> 115

<211> 382

<212> PRT

<213> Homo sapiens

<400> 115

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Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln Ala
 1               5                  10                  15

Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe Ile Phe
               20                  25                  30

Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp Gly Asp Glu
               35                  40                  45

Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val
           50                  55                  60

Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val Arg Phe Trp Val Leu
 65              70                  75                  80

Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu Tyr Leu Ala His Val
               85                  90                  95

Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn Lys Lys Glu Glu Glu
               100                 105                 110

Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
               115                 120                 125

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
           130                 135                 140

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
145                 150                 155                 160
```

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
         165   170   175

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
         180   185   190

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
         195   200   205

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
210   215   220

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
225   230   235   240

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
         245   250   255

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
         260   265   270

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
         275   280   285

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
         290   295   300

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met

```
305                    310                    315                    320
```

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
```
              325                    330                    335
```

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
```
              340                    345                    350
```

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
```
              355                    360                    365
```

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
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              370                    375                    380
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<210> 116

<211> 3074

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (201)..(1346)

<400> 116

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aacagcagcg gagtttTaaa ctttaaatag acaggtctga gtgcctgaac ttgcctttTc 120

attttacttc atcctccaag gagttcaatc acttggcgtg acttcactac ttttaagcaa 180

aagagtggtg cccaggcaac atg ggt gac tgg agc gcc tta ggc aaa ctc ctt 233
                         Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu
                         1   5   10

gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg ctg tca 281
Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser
        15   20   25

gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt gag tca 329
Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser
     30   35   40

gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag caa cct 377
Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro
     45   50   55

ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct cat gtg 425
Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val
60   65   70   75

cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca ctc ttg 473
Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr Leu Leu
        80   85   90

tac ctg gct cat gtg ttc tat gtg atg cga aag gaa gag aaa ctg aac 521
Tyr Leu Ala His Val Phe Tyr Val Met Arg Lys Glu Glu Lys Leu Asn
        95   100   105

aag aaa gag gaa gaa ctc aag gtt gcc caa act gat ggt gtc aat gtg   569
Lys Lys Glu Glu Glu Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val
      110   115   120

gac atg cac ttg aag cag att gag ata aag aag ttc aag tac ggt att   617
Asp Met His Leu Lys Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile
      125   130   135

gaa gag cat ggt aag gtg aaa atg cga ggg ggg ttg ctg cga acc tac   665
Glu Glu His Gly Lys Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr
140   145   150   155

atc atc agt atc ctc ttc aag tct atc ttt gag gtg gcc ttc ttg ctg   713
Ile Ile Ser Ile Leu Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu
            160   165   170

atc cag tgg tac atc tat gga ttc agc ttg agt gct gtt tac act tgc   761
Ile Gln Trp Tyr Ile Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys
            175   180   185

aaa aga gat ccc tgc cca cat cag gtg gac tgt ttc ctc tct cgc ccc   809
Lys Arg Asp Pro Cys Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro
            190   195   200

acg gag aaa acc atc ttc atc atc ttc atg ctg gtg gtg tcc ttg gtg   857
Thr Glu Lys Thr Ile Phe Ile Ile Phe Met Leu Val Val Ser Leu Val
      205   210   215

tcc ctg gcc ttg aat atc att gaa ctc ttc tat gtt ttc ttc aag ggc   905
Ser Leu Ala Leu Asn Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly
220   225   230   235

gtt aag gat cgg gtt aag gga aag agc gac cct tac cat gcg acc agt   953
Val Lys Asp Arg Val Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser
                240   245   250

ggt gcg ctg agc cct gcc aaa gac tgt ggg tct caa aaa tat gct tat   1001
Gly Ala Leu Ser Pro Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr
                255   260   265

ttc aat ggc tgc tcc tca cca acc gct ccc ctc tcg cct atg tct cct   1049
Phe Asn Gly Cys Ser Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro
                270   275   280

cct ggg tac aag ctg gtt act ggc gac aga aac aat tct tct tgc cgc   1097
Pro Gly Tyr Lys Leu Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg
        285   290   295

aat tac aac aag caa gca agt gag caa aac tgg gct aat tac agt gca   1145
Asn Tyr Asn Lys Gln Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala
300   305   310   315

gaa caa aat cga atg ggg cag gcg gga agc acc atc tct aac tcc cat   1193
Glu Gln Asn Arg Met Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His
                320   325   330

gca cag cct ttt gat ttc ccc gat gat aac cag aat tct aaa aaa cta   1241

```
Ala Gln Pro Phe Asp Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu
         335             340             345
```

```
gct gct gga cat gaa tta cag cca cta gcc att gtg gac cag cga cct   1289
Ala Ala Gly His Glu Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro
         350             355             360
```

```
tca agc aga gcc agc agt cgt gcc agc agc aga cct cgg cct gat gac   1337
Ser Ser Arg Ala Ser Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp
         365             370             375
```

```
ctg gag atc tagatacagg cttgaaagca tcaagattcc actcaattgt          1386
Leu Glu Ile
380
```

```
ggagaagaaa aaaggtgctg tagaaagtgc accaggtgtt aattttgatc cggtggaggt 1446
```

```
ggtactcaac agccttattc atgaggctta gaaaacacaa agacattaga atacctaggt 1506
```

```
tcactggggg tgtatggggt agatgggtgg agagggaggg gataagagag gtgcatgttg 1566
```

```
gtatttaaag tagtggattc aaagaactta gattataaat aagagttcca ttaggtgata 1626
```

```
catagataag ggctttttct ccccgcaaac acccctaaga atggttctgt gtatgtgaat 1686
```

```
gagcgggtgg taattgtggc taaatatttt tgttttacca agaaactgaa ataattctgg 1746
```

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ccaggaataa atacttcctg aacatcttag gtcttttcaa caagaaaaag acagaggatt 1806
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gtccttaagt ccctgctaaa acattccatt gttaaaattt gcactttgaa ggtaagcttt 1866

ctaggcctga ccctccaggt gtcaatggac ttgtgctact atattttttt attcttggta 1926

tcagtttaaa attcagacaa ggcccacaga ataagatttt ccatgcattt gcaaatacgt 1986

atattctttt tccatccact tgcacaatat cattaccatc acttttttcat cattcctcag 2046

ctactactca cattcattta atggtttctg taaacatttt taagacagtt gggatgtcac 2106

ttaacatttt tttttgagc taaagtcagg gaatcaagcc atgcttaata tttaacaatc 2166

acttatatgt gtgtcgaaga gtttgttttg tttgtcatgt attggtacaa gcagatacag 2226

tataaactca caaacacaga tttgaaaata atgcacatat ggtgttcaaa tttgaacctt 2286

tctcatggat ttttgtggtg tgggccaata tggtgtttac attatataat tcctgctgtg 2346

gcaagtaaag cacacttttt ttttctccta aaatgttttt ccctgtgtat cctattatgg 2406

atactggttt tgttaattat gattctttat tttctctcct tttttttagga tatagcagta 2466

atgctattac tgaaatgaat ttcctttttc tgaaatgtaa tcattgatgc ttgaatgata 2526

gaattttagt actgtaaaca ggctttagtc attaatgtga gagacttaga aaaaaatgct 2586

tagagtggac tattaaatgt gcctaaatga attttgcagt aactggtatt cttgggtttt 2646

cctacttaat acacagtaat tcagaacttg tattctatta tgagtttagc agtctttttgg 2706

agtgaccagc aactttgatg tttgcactaa gattttattt ggaatgcaag agaggttgaa 2766

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cagtttctcc aaatgccttt tttaaaactc atcacagaag attggtgaaa atgctgagta 2886

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ctaatttgtt tgacattcca tgttaaacta cggtcatgtt cagcttcatt gcatgtaatg 3006

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tttagtat   3074

<210> 117

<211> 398

<212> PRT

<213> Homo sapiens

<400> 117

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1   5   10   15

Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu Glu Ala Gly Ala
                20   25   30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln

```
          35                    40                    45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
      50                    55                    60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65                    70                    75                    80

Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
                    85                    90                    95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
           100                   105                   110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
           115                   120                   125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
           130                   135                   140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145                   150                   155                   160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
                    165                   170                   175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
                    180                   185                   190
```

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
　　　　195　　　　　　　　　　200　　　　　　　　　205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
　　210　　　　　　　　　　215　　　　　　　　　220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225　　　　　　　　　　230　　　　　　　　235　　　　　　　　　240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
　　　　　　　　　　245　　　　　　　　250　　　　　　　　　255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
　　　　　　　　260　　　　　　　　265　　　　　　　　　270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
　　　　275　　　　　　　　　280　　　　　　　　285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
　　　　290　　　　　　　　　295　　　　　　　　300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305　　　　　　　　　　310　　　　　　　　315　　　　　　　　　320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
　　　　　　　　325　　　　　　　　330　　　　　　　　　335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
　　　　340　　　　　　　　　345　　　　　　　　350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
     355   360   365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
     370   375   380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu
     385   390   395

<210> 118

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 118

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg 60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc 111
               Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
                1   5   10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga gtg agg gca gag 159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly Val Arg Ala Glu

```
                15                    20                    25


gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act   207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
        30                    35                    40


gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg   255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met
    45                    50                    55                    60


gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag   303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
                    65                    70                    75


gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag   351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
                80                    85                    90


gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca   399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
                95                    100                   105


gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg   447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
    110                   115                   120


aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt   495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125                   130                   135                   140
```

ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga 543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
             145   150   155

agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc 591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
             160   165   170

acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc 639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
             175   180   185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc 687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
             190   195   200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg 735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205   210   215   220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca 783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
             225   230   235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag 831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
             240   245   250

```
gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta        879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
        255             260             265


gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt        927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
        270             275             280


gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca        975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285             290             295             300


gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa       1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
                305             310             315


cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga       1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
                320             325             330


gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat       1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
                335             340             345


gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag       1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
        350             355             360


tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag       1215
```

```
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
365             370             375             380


aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa   1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
                385             390             395


gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg cagggggcca    1319
Glu Leu


ggacaaaatg caaacttttt tttttctga dacagagtct tgctctgtcg ccaagttgca   1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa   1439

aaaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc    1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt   1559

tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc   1619

cgaagaatga agtctttccc tggtgatggt cccctgccct gtctttccag catccactct   1679

cccttgtcct cctggggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg   1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga   1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct   1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct   1919
```

cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatc   2054

<210> 119

<211> 398

<212> PRT

<213> Homo sapiens

<400> 119

Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
1   5   10   15

Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
                20   25   30

Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
            35   40   45

Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
        50   55   60

Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
65   70   75   80

Thr Gln Asn Leu Leu Leu Leu Thr Asp Asn Glu Ala Trp Asn Gly
                85   90   95

Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala Asp Glu Leu Arg
            100   105   110

Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met Lys Asp Lys Asn
            115   120   125

Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe Leu Lys Glu Phe
        130   135   140

Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg Arg Leu Arg Ala
145   150   155   160

Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr Thr Ile Ala Asn
            165   170   175

Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile Leu Thr Leu Val
            180   185   190

Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser Leu Val Leu Leu
            195   200   205

Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu Thr Gly Ile Thr
            210   215   220

Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr Gln Ala Gln Ala
225   230   235   240

His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys Glu Val Lys Glu
          245   250   255

Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu Ala Gly Asn Thr
          260   265   270

Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg Ala Leu Arg Arg
          275   280   285

Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser Ala Ser Arg Pro
          290   295   300

Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu Gln Val Glu Arg
305   310   315   320

Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly Val Lys Leu Thr
          325   330   335

Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp Val Val Tyr Leu
          340   345   350

Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys Ser Glu Thr Ala
          355   360   365

Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu Lys Leu Asn Ile
          370   375   380

Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln Glu Leu

385   390   395

<210> 120

<211> 2054

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(1269)

<400> 120

cacacagctc agaacagctg gatcttgctc agtctctgcc aggggaagat tccttggagg   60

aggccctgca gcgac atg gag gga gct gct ttg ctg aga gtc tct gtc ctc   111
                 Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu
                 1   5   10

tgc atc tgg atg agt gca ctt ttc ctt ggt gtg aga gtg agg gca gag   159
Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu
       15   20   25

gaa gct gga gcg agg gtg caa caa aac gtt cca agt ggg aca gat act   207
Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr
    30   35   40

gga gat cct caa agt aag ccc ctc ggt gac tgg gct gct ggc acc atg   255
Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met

45　　　　　　　　　　　50　　　　　　　　　　　55　　　　　　　　　　　60

```
gac cca gag agc agt atc ttt att gag gat gcc att aag tat ttc aag    303
Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys
                    65                  70                  75


gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg act gat aat gag    351
Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu Leu Thr Asp Asn Glu
                80                  85                  90


gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc agg aat gag gca    399
Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro Arg Asn Glu Ala
            95                  100                 105


gat gag ctc cgt aaa gct ctg gac aac ctt gca aga caa atg atc atg    447
Asp Glu Leu Arg Lys Ala Leu Asp Asn Leu Ala Arg Gln Met Ile Met
        110                 115                 120


aaa gac aaa aac tgg cac gat aaa ggc cag cag tac aga aac tgg ttt    495
Lys Asp Lys Asn Trp His Asp Lys Gly Gln Gln Tyr Arg Asn Trp Phe
125                 130                 135                 140


ctg aaa gag ttt cct cgg ttg aaa agt aag ctt gag gat aac ata aga    543
Leu Lys Glu Phe Pro Arg Leu Lys Ser Lys Leu Glu Asp Asn Ile Arg
                145                 150                 155


agg ctc cgt gcc ctt gca gat ggg gtt cag aag gtc cac aaa ggc acc    591
Arg Leu Arg Ala Leu Ala Asp Gly Val Gln Lys Val His Lys Gly Thr
            160                 165                 170
```

```
acc atc gcc aat gtg gtg tct ggc tct ctc agc att tcc tct ggc atc    639
Thr Ile Ala Asn Val Val Ser Gly Ser Leu Ser Ile Ser Ser Gly Ile
        175             180             185

ctg acc ctc gtc ggc atg ggt ctg gca ccc ttc aca gag gga ggc agc    687
Leu Thr Leu Val Gly Met Gly Leu Ala Pro Phe Thr Glu Gly Gly Ser
    190             195             200

ctt gta ctc ttg gaa cct ggg atg gag ttg gga atc aca gca gct ttg    735
Leu Val Leu Leu Glu Pro Gly Met Glu Leu Gly Ile Thr Ala Ala Leu
205             210             215             220

acc ggg att acc agc agt acc ata gac tac gga aag aag tgg tgg aca    783
Thr Gly Ile Thr Ser Ser Thr Ile Asp Tyr Gly Lys Lys Trp Trp Thr
            225             230             235

caa gcc caa gcc cac gac ctg gtc atc aaa agc ctt gac aaa ttg aag    831
Gln Ala Gln Ala His Asp Leu Val Ile Lys Ser Leu Asp Lys Leu Lys
            240             245             250

gag gtg aag gag ttt ttg ggt gag aac ata tcc aac ttt ctt tcc tta    879
Glu Val Lys Glu Phe Leu Gly Glu Asn Ile Ser Asn Phe Leu Ser Leu
        255             260             265

gct ggc aat act tac caa ctc aca cga ggc att ggg aag gac atc cgt    927
Ala Gly Asn Thr Tyr Gln Leu Thr Arg Gly Ile Gly Lys Asp Ile Arg
        270             275             280
```

```
gcc ctc aga cga gcc aga gcc aat ctt cag tca gta ccg cat gcc tca      975
Ala Leu Arg Arg Ala Arg Ala Asn Leu Gln Ser Val Pro His Ala Ser
285             290         295             300


gcc tca cgc ccc cgg gtc act gag cca atc tca gct gaa agc ggt gaa      1023
Ala Ser Arg Pro Arg Val Thr Glu Pro Ile Ser Ala Glu Ser Gly Glu
            305             310             315


cag gtg gag aga gtt aat gaa ccc agc atc ctg gaa atg agc aga gga      1071
Gln Val Glu Arg Val Asn Glu Pro Ser Ile Leu Glu Met Ser Arg Gly
            320             325             330


gtc aag ctc acg gat gtg gcc cct gta agc ttc ttt ctt gtg ctg gat      1119
Val Lys Leu Thr Asp Val Ala Pro Val Ser Phe Phe Leu Val Leu Asp
            335             340             345


gta gtc tac ctc gtg tac gaa tca aag cac tta cat gag ggg gca aag      1167
Val Val Tyr Leu Val Tyr Glu Ser Lys His Leu His Glu Gly Ala Lys
            350             355             360


tca gag aca gct gag gag ctg aag aag gtg gct cag gag ctg gag gag      1215
Ser Glu Thr Ala Glu Glu Leu Lys Lys Val Ala Gln Glu Leu Glu Glu
365             370             375             380


aag cta aac att ctc aac aat aat tat aag att ctg cag gcg gac caa      1263
Lys Leu Asn Ile Leu Asn Asn Asn Tyr Lys Ile Leu Gln Ala Asp Gln
            385             390             395


gaa ctg tgaccacagg gcagggcagc caccaggaga gatatgcctg gcaggggcca      1319
Glu Leu
```

Glu Leu

ggacaaaatg caaactttt tttttctga gacagagtct tgctctgtcg ccaagttgca 1379

gtgagccgag atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa 1439

aaaaaaaaaa aaaagaata tattgacgga agaatagaga ggaggcttga aggaaccagc 1499

aatgagaagg ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt 1559

tggatacagg agaagaaaca gcggctccac tacagaccca gccccaggtt caatgtcctc 1619

cgaagaatga agtctttccc tggtgatggt cccctgccct gtctttccag catccactct 1679

cccttgtcct cctgggggca tatctcagtc aggcagcggc ttcctgatga tggtcgttgg 1739

ggtggttgtc atgtgatggg tcccctccag gttactaaag ggtgcatgtc ccctgcttga 1799

acactgaagg gcaggtggtg agccatggcc atggtcccca gctgaggagc aggtgtccct 1859

gagaacccaa acttcccaga gagtatgtga gaaccaacca atgaaaacag tcccatcgct 1919

cttacccggt aagtaaacag tcagaaaatt agcatgaaag cagtttagca ttgggaggaa 1979

gctcagatct ctagagctgt cttgtccccg cccaggattg acctgtgtaa gtcccaataa 2039

actcacctac tcatc   2054

<210> 121

<211> 108

<212> PRT

<213> Homo sapiens

<400> 121

Met Gly Val Gln Val Glu Thr Ile Ser Pro Gly Asp Gly Arg Thr Phe

1   5   10   15

Pro Lys Arg Gly Gln Thr Cys Val Val His Tyr Thr Gly Met Leu Glu

            20   25   30

Asp Gly Lys Lys Phe Asp Ser Ser Arg Asp Arg Asn Lys Pro Phe Lys

            35   40   45

Phe Met Leu Gly Lys Gln Glu Val Ile Arg Gly Trp Glu Glu Gly Val

        50   55   60

Ala Gln Met Ser Val Gly Gln Arg Ala Lys Leu Thr Ile Ser Pro Asp

65   70   75   80

Tyr Ala Tyr Gly Ala Thr Gly His Pro Gly Ile Ile Pro Pro His Ala

            85   90   95

Thr Leu Val Phe Asp Val Glu Leu Leu Lys Leu Glu

            100   105

<210> 122

<211> 1546

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)..(412)

<400> 122

actaggcaga gccgtggaac cgccgccagg tcgctgttgg tccacgccgc ccgtcgcgcc 60

gcccgcccgc tcagcgtccg ccgccgcc atg gga gtg cag gtg gaa acc atc   112
                                Met Gly Val Gln Val Glu Thr Ile
                                 1   5

tcc cca gga gac ggg cgc acc ttc ccc aag cgc ggc cag acc tgc gtg   160
Ser Pro Gly Asp Gly Arg Thr Phe Pro Lys Arg Gly Gln Thr Cys Val
   10   15   20

gtg cac tac acc ggg atg ctt gaa gat gga aag aaa ttt gat tcc tcc   208
Val His Tyr Thr Gly Met Leu Glu Asp Gly Lys Lys Phe Asp Ser Ser
 25   30   35   40

cgg gac aga aac aag ccc ttt aag ttt atg cta ggc aag cag gag gtg   256
Arg Asp Arg Asn Lys Pro Phe Lys Phe Met Leu Gly Lys Gln Glu Val
                45   50   55

atc cga ggc tgg gaa gaa ggg gtt gcc cag atg agt gtg ggt cag aga   304
Ile Arg Gly Trp Glu Glu Gly Val Ala Gln Met Ser Val Gly Gln Arg

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            60                    65                    70

gcc aaa ctg act ata tct cca gat tat gcc tat ggt gcc act ggg cac    352
Ala Lys Leu Thr Ile Ser Pro Asp Tyr Ala Tyr Gly Ala Thr Gly His
            75                    80                    85


cca ggc atc atc cca cca cat gcc act ctc gtc ttc gat gtg gag ctt    400
Pro Gly Ile Ile Pro Pro His Ala Thr Leu Val Phe Asp Val Glu Leu
            90                    95                   100


cta aaa ctg gaa tgacaggaat ggcctcctcc cttagctccc tgttcttgga        452
Leu Lys Leu Glu
105


tctgccatgg agggatctgg tgcctccaga catgtgcaca tgaatccata tggagctttt  512


cctgatgttc cactccactt tgtatagaca tctgccctga ctgaatgtgt tctgtcactc  572


agctttgctt ccgacacctc tgtttcctct tccccttct cctcgtatgt gtgtttacct   632


aaactatatg ccataaacct caagttactc attttatttt gttttcattt tggggtgaag  692


attcagtttc agtcttttgg atataggttt ccaattaagt acatggtcaa gtattaacag  752


cacaagtggt aggttaacat tagaatagga attggtgttg ggggggggt ttgcaagaat   812


attttatttt aatttttgg atgaaatttt tatctattat atattaaaca ttcttgctgc   872


tgcgctgcaa agccatagca gatttgaggc gctgttgagg actgaattac tctccaagtt  932
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gagagatgtc tttgggttaa attaaaagcc ctacctaaaa ctgaggtggg gatggggaga 992

gcctttgcct ccaccattcc cacccaccct ccccttaaac cctctgcctt tgaaagtaga 1052

tcatgttcac tgcaatgctg gacactacag gtatctgtcc ctgggccagc agggacctct 1112

gaagccttct ttgtggcctt tttttttttt tcatcctgtg gtttttctaa tggactttca 1172

ggaattttgt aatctcataa ctttccaagc tccaccactt cctaaatctt aagaacttta 1232

attgacagtt tcaattgaag gtgctgtttg tagacttaac acccagtgaa agcccagcca 1292

tcatgacaaa tccttgaatg ttctcttaag aaaatgatgc tggtcatcgc agcttcagca 1352

tctcctgttt tttgatgctt ggctccctct gctgatctca gtttcctggc ttttcctccc 1412

tcagcccctt ctcacccctt tgctgtcctg tgtagtgatt tggtgagaaa tcgttgctgc 1472

acccttcccc cagcaccatt tatgagtctc aagttttatt attgcaataa aagtgcttta 1532

tgccggcttt tctc   1546

<210> 123

<211> 679

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala Thr Ala Ala Ser Gly
1   5   10   15

Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu Gly Phe Ile Ile Ala
            20   25   30

Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser Phe
            35   40   45

Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys Ile
    50   55   60

Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val Leu Leu Gly Ala Lys
65   70   75   80

Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp Val Glu Met Tyr Asn
                85   90   95

Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe Gly
                100   105   110

Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile Ser
            115   120   125

Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val Ala
            130   135   140

Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val Met

145   150   155   160

Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile Leu
               165   170   175

Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys Ala Asp Pro Val Pro
               180   185   190

Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala Cys Thr Val Gly Ile
               195   200   205

Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe Asp
             210   215   220

Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala Val
225   230   235   240

Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys Arg
               245   250   255

Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser Glu Ser Pro Leu Met
               260   265   270

Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu Glu Thr Lys Leu Ser
               275   280   285

Val Gly Asp Ile Glu Asn Lys His Pro Val Ser Glu Val Gly Pro Ala
             290   295   300

Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg Thr Val Ser Phe Lys
305   310   315   320

Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Ser Val
                325   330   335

Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Val Asn Gly Ala Val
                340   345   350

Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Ala Val Ser Asn
                355   360   365

Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
        370   375   380

Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
385   390   395   400

Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
                405   410   415

Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
                420   425   430

Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu Glu Met Glu Lys Leu
                435   440   445

Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile Arg Met Asp Ser Tyr
        450   455   460

Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Ala Ser Glu Ile
465   470   475   480

Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
                485   490   495

Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
                500   505   510

Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
                515   520   525

Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
        530   535   540

Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser Ser Lys Val Ala Thr
545   550   555   560

Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Val Gly Leu
                565   570   575

Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr
                580   585   590

Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu
                595   600   605

Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His

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         610                  615                  620

Cys Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys
625                  630                  635                  640


Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val
                    645                  650                  655


Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Ile Phe
                         660                  665                  670


Arg Tyr Val Ile Leu Arg Met
                   675
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<210> 124

<211> 2916

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(2117)

<400> 124

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aacaaccact actccagaga atg gca acg ctg att acc agt act aca gct gct 113
                       Met Ala Thr Leu Ile Thr Ser Thr Thr Ala Ala
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```
               1                 5                      10

acc gcc gct tct ggt cct ttg gtg gac tac cta tgg atg ctc atc ctg   161
Thr Ala Ala Ser Gly Pro Leu Val Asp Tyr Leu Trp Met Leu Ile Leu
            15                  20                  25


ggc ttc att att gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat   209
Gly Phe Ile Ile Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp
            30                  35                  40


gta gca aat tct ttt ggt aca gct gtg ggc tca ggt gta gtg acc ctg   257
Val Ala Asn Ser Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu
            45                  50                  55


aag caa gcc tgc atc cta gct agc atc ttt gaa aca gtg ggc tct gtc   305
Lys Gln Ala Cys Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Val
     60                  65                  70                  75


tta ctg ggg gcc aaa gtg agc gaa acc atc cgg aag ggc ttg att gac   353
Leu Leu Gly Ala Lys Val Ser Glu Thr Ile Arg Lys Gly Leu Ile Asp
                 80                  85                  90


gtg gag atg tac aac tcg act caa ggg ctg ctg atg gcc ggc tca gtc   401
Val Glu Met Tyr Asn Ser Thr Gln Gly Leu Leu Met Ala Gly Ser Val
            95                  100                 105


agt gct atg ttt ggt tct gct gtg tgg caa ctc gtg gct tcg ttt ttg   449
Ser Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu
            110                 115                 120
```

aag ctc cct att tct gga acc cat tgt att gtt ggt gca act att ggt 497
Lys Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly
　　125　　　　　　　　　130　　　　　　　　135

ttc tcc ctc gtg gca aag ggg cag gag ggt gtc aag tgg tct gaa ctg 545
Phe Ser Leu Val Ala Lys Gly Gln Glu Gly Val Lys Trp Ser Glu Leu
140　　　　　　　　145　　　　　　　　150　　　　　　　　155

ata aaa att gtg atg tct tgg ttc gtg tcc cca ctg ctt tct gga att 593
Ile Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile
　　　　　　　160　　　　　　　　165　　　　　　　170

atg tct gga att tta ttc ttc ctg gtt cgt gca ttc atc ctc cat aag 641
Met Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu His Lys
　　　　　　175　　　　　　　　180　　　　　　　　185

gca gat cca gtt cct aat ggt ttg cga gct ttg cca gtt ttc tat gcc 689
Ala Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Val Phe Tyr Ala
　　190　　　　　　　　195　　　　　　　　200

tgc aca gtt gga ata aac ctc ttt tcc atc atg tat act gga gca ccg 737
Cys Thr Val Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro
　　205　　　　　　　　210　　　　　　　　215

ttg ctg ggc ttt gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg 785
Leu Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser
220　　　　　　　　225　　　　　　　　230　　　　　　　　235

```
gtg gga tgt gca gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt      833
Val Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys
                240             245             250


ccc agg atg aag aga aaa att gaa cga gaa ata aag tgt agt cct tct      881
Pro Arg Met Lys Arg Lys Ile Glu Arg Glu Ile Lys Cys Ser Pro Ser
                255             260             265


gaa agc ccc tta atg gaa aaa aag aat agc ttg aaa gaa gac cat gaa      929
Glu Ser Pro Leu Met Glu Lys Lys Asn Ser Leu Lys Glu Asp His Glu
                270             275             280


gaa aca aag ttg tct gtt ggt gat att gaa aac aag cat cct gtt tct      977
Glu Thr Lys Leu Ser Val Gly Asp Ile Glu Asn Lys His Pro Val Ser
                285             290             295


gag gta ggg cct gcc act gtg ccc ctc cag gct gtg gtg gag gag aga      1025
Glu Val Gly Pro Ala Thr Val Pro Leu Gln Ala Val Val Glu Glu Arg
300             305             310             315


aca gtc tca ttc aaa ctt gga gat ttg gag gaa gct cca gag aga gag      1073
Thr Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu
                320             325             330


agg ctt ccc agc gtg gac ttg aaa gag gaa acc agc ata gat agc acc      1121
Arg Leu Pro Ser Val Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr
                335             340             345


gtg aat ggt gca gtg cag ttg cct aat ggg aac ctt gtc cag ttc agt      1169
```

Val Asn Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser
     350   355   360

caa gcc gtc agc aac caa ata aac tcc agt ggc cac tac cag tat cac   1217
Gln Ala Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His
     365   370   375

acc gtg cat aag gat tcc ggc ctg tac aaa gag cta ctc cat aaa tta   1265
Thr Val His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu
     380   385   390   395

cat ctt gcc aag gtg gga gat tgc atg gga gac tcc ggt gac aaa ccc   1313
His Leu Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro
            400   405   410

tta agg cgc aat aat agc tat act tcc tat acc atg gca ata tgt ggc   1361
Leu Arg Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly
            415   420   425

atg cct ctg gat tca ttc cgt gcc aaa gaa ggt gaa cag aag ggc gaa   1409
Met Pro Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Glu
            430   435   440

gaa atg gag aag ctg aca tgg cct aat gca gac tcc aag aag cga att   1457
Glu Met Glu Lys Leu Thr Trp Pro Asn Ala Asp Ser Lys Lys Arg Ile
     445   450   455

cga atg gac agt tac acc agt tac tgc aat gct gtg tct gac ctt cac   1505
Arg Met Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His

460   465   470   475

tca gca tct gag ata gac atg agt gtc aag gca gag atg ggt cta ggt   1553
Ser Ala Ser Glu Ile Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly
                480   485   490

gac aga aaa gga agt aat ggc tct cta gaa gaa tgg tat gac cag gat   1601
Asp Arg Lys Gly Ser Asn Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp
                    495   500   505

aag cct gaa gtc tct ctc ctc ttc cag ttc ctg cag atc ctt aca gcc   1649
Lys Pro Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala
           510   515   520

tgc ttt ggg tca ttc gcc cat ggt ggc aat gac gta agc aat gcc att   1697
Cys Phe Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile
           525   530   535

ggg cct ctg gtt gct tta tat ttg gtt tat gac aca gga gat gtt tct   1745
Gly Pro Leu Val Ala Leu Tyr Leu Val Tyr Asp Thr Gly Asp Val Ser
540   545   550   555

tca aaa gtg gca aca cca ata tgg ctt cta ctc tat ggt ggt gtt ggt   1793
Ser Lys Val Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly
                560   565   570

atc tgt gtt ggt ctg tgg gtt tgg gga aga aga gtt atc cag acc atg   1841
Ile Cys Val Gly Leu Trp Val Trp Gly Arg Arg Val Ile Gln Thr Met
           575   580   585

```
ggg aag gat ctg aca ccg atc aca ccc tct agt ggc ttc agt att gaa    1889
Gly Lys Asp Leu Thr Pro Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu
        590               595               600


ctg gca tct gcc ctc act gtg gtg att gca tca aat att ggc ctt ccc    1937
Leu Ala Ser Ala Leu Thr Val Val Ile Ala Ser Asn Ile Gly Leu Pro
        605               610               615


atc agt aca aca cat tgt aaa gtg ggc tct gtt gtg tct gtt ggc tgg    1985
Ile Ser Thr Thr His Cys Lys Val Gly Ser Val Val Ser Val Gly Trp
620               625               630               635


ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt    2033
Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe
            640               645               650


atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc    2081
Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala
        655               660               665


atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt         2127
Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met
        670               675


tgagattaaa atttgtgtca atgtttggga ccatcttagg tattcctgct cccctgaaga  2187


atgattacag tgttaacaga agactgacaa gagtcttttt atttgggagc cagaggaggg  2247
```

```
aagtgttact tgtgctataa ctgctttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct acttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gattttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa ctttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatggat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaatggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agttttttag                                                        2916
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<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met	Glu	Arg	Pro	Gln	Pro	Asp	Ser	Met	Pro	Gln	Asp	Leu	Ser	Glu	Ala
1				5					10					15	

Leu	Lys	Glu	Ala	Thr	Lys	Glu	Val	His	Thr	Gln	Ala	Glu	Asn	Ala	Glu
			20					25				30			

Phe	Met	Arg	Asn	Phe	Gln	Lys	Gly	Gln	Val	Thr	Arg	Asp	Gly	Phe	Lys
		35				40					45				

Leu	Val	Met	Ala	Ser	Leu	Tyr	His	Ile	Tyr	Val	Ala	Leu	Glu	Glu	Glu
	50				55				60						

Ile	Glu	Arg	Asn	Lys	Glu	Ser	Pro	Val	Phe	Ala	Pro	Val	Tyr	Phe	Pro
65				70				75				80			

Glu	Glu	Leu	His	Arg	Lys	Ala	Ala	Leu	Glu	Gln	Asp	Leu	Ala	Phe	Trp
				85				90				95			

Tyr	Gly	Pro	Arg	Trp	Gln	Glu	Val	Ile	Pro	Tyr	Thr	Pro	Ala	Met	Gln
			100				105					110			

Arg	Tyr	Val	Lys	Arg	Leu	His	Glu	Val	Gly	Arg	Thr	Glu	Pro	Glu	Leu
		115				120					125				

Leu	Val	Ala	His	Ala	Tyr	Thr	Arg	Tyr	Leu	Gly	Asp	Leu	Ser	Gly	Gly
	130				135				140						

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145   150   155   160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
                   165   170   175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
                   180   185   190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
                   195   200   205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp
          210   215   220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala
225   230   235   240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys
                   245   250   255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu
                   260   265   270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met
                   275   280   285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(944)

<400> 126

tcaacgcctg cctcccctcg agcgtcctca gcgcagccgc cgcccgcgga gccagcacga   60

acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag   113
                       Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln
                        1   5   10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag   161
Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln
              15   20   25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc   209
Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr
         30   35   40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg   257
Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val
         45   50   55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc   305
Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

```
      60                    65                    70                    75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag    353
Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln
                80                    85                    90


gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac    401
Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr
                95                    100                   105


aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc    449
Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg
           110                   115                   120


aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt    497
Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly
           125                   130                   135


gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg    545
Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu
140                   145                   150                   155


gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac    593
Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn
                160                   165                   170


att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac    641
Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn
                175                   180                   185
```

```
tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc    689
Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala
      190                 195                 200


aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag    737
Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu
      205                 210                 215


ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg    785
Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly
220                 225                 230                 235


ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag    833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu
                  240                 245                 250


act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt    881
Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu
            255                 260                 265


ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta    929
Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val
      270                 275                 280


ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt    984
Gly Leu Tyr Ala Met
      285
```

ccggtggaag gccttctttc tagagaggga attctcttgg ctggcttcct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcatcttccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acaccctaat gtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttggagcc actctgttcc tggctcagcc 1404

tcaaatgcag tattttttgtt gtgttctgtt gttttatag cagggttggg gtggtttttg 1464

agccatgcgt gggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg   1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1   5   10   15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val
             20   25   30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro
             35   40   45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys
             50   55   60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe
 65   70   75   80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn
                 85   90   95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg
                100   105   110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys
             115   120   125

Ile Lys Cys Val Ala Phe Asp
             130   135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

cttctgacag ctggtgcgcc tgcccgggaa catcctcctg gactcaatc atg gct tgt 58

Met Ala Cys

1

```
ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga    106
Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg
        5                  10                  15
```

```
gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg    154
Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu
 20                  25                  30                  35
```

```
ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac    202
Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn
                40                  45                  50
```

```
gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggg    250
Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly
                55                  60                  65
```

```
gcc tgg ggg acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga    298
Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly
```

```
                70                    75                    80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc    346
Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val
            85                    90                    95


aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg    394
Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu
100               105               110               115


gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt    442
Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys
                  120               125               130


gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc    494
Val Ala Phe Asp
            135


ctctgctccc ctg                                                      507
```

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

```
Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn
1               5                     10                    15
```

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn
            20   25   30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp
            35   40   45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys
            50   55   60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser
65   70   75   80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
                    85   90   95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
                100   105   110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
                115   120   125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
                130   135   140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145   150   155   160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro

```
                165                 170                 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
                180                 185                 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
                195                 200                 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
            210                 215                 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225                 230                 235                 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
                245                 250                 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
                260                 265                 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
            275                 280                 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
            290                 295                 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
305                 310                 315                 320
```

出証特２００２－３０３２９３５

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
                325   330   335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
                340   345   350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
                355   360   365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
        370   375   380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp
385   390   395   400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu
                405   410   415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe
                420   425   430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn
                435   440   445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile
        450   455   460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp
465   470   475   480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu
         485   490   495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser
         500   505   510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr
         515   520   525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn
         530   535   540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545   550   555   560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
         565   570   575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
         580   585   590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
         595   600   605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
         610   615   620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn

```
          625                 630                 635                 640
```

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg

```
                        645                 650                 655
```

Leu Arg Ile Ser Glu Lys

```
                        660
```


<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(2059)

<400> 130

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tcagtggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag   109
            Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu
            1   5   10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt   157
Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys
        15   20   25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg   205
Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu
    30   35   40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc   253
Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val
    45   50   55   60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg   301
Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu
           65   70   75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct   349
Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro
           80   85   90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag   397
Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu
           95   100   105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga   445
Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly
     110   115   120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag   493
Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys
125   130   135   140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act   541

Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr
            145   150   155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca   589
Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr
            160   165   170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat   637
Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn
            175   180   185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg   685
Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val
            190   195   200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca   733
Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser
205   210   215   220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt   781
Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe
            225   230   235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga   829
Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly
            240   245   250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct   877
His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

```
                255                      260                      265


cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg    925
Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu
        270                      275                  280


aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat    973
Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp
285                  290                      295                  300


atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat    1021
Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp
                    305                      310                  315


gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa    1069
Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln
                    320                      325                  330


gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc    1117
Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile
            335                      340                  345


ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act    1165
Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr
        350                      355                      360


gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc    1213
Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr
365                  370                      375                  380
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aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga    1261
Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg
            385                 390                 395


gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt    1309
Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu
            400                 405                 410


gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg    1357
Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met
        415                 420                 425


tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct    1405
Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala
        430                 435                 440


gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca    1453
Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro
445                 450                 455                 460


ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat    1501
Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp
                465                 470                 475


cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act    1549
Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr
                480                 485                 490
```

```
ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc      1597
Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr
        495                 500                 505


aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta      1645
Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val
        510                 515                 520


tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag      1693
Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys
525                 530                 535                 540


cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat      1741
Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His
            545                 550                 555


cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat      1789
Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn
            560                 565                 570


ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat      1837
Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr
            575                 580                 585


cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt      1885
His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly
        590                 595                 600


aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act      1933
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Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr
605             610             615             620


cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt    1981
Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe
            625             630             635


agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt    2029
Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser
            640             645             650


ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gttttttgaaa    2079
Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys
            655             660


gttagcataa ttttagatgc ctgtgaaata gtactgcact tacataaagt gagacattgt 2139


gaaaaggcaa atttgtatat gtagagaaag aatagtagta actgtttcat agcaaacttc 2199


aggactttga gatgttgaaa ttacattatt taattacaga cttcctcttt ct         2251
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<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

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     1                  5                    10                      15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg
                20                    25                    30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala
                35                    40                    45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
                50                    55                    60

Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
    65                  70                   75                      80

Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
                85                    90                    95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
                100                   105                   110

Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
                115                   120                   125

Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
                130                   135                   140

Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
    145                 150                   155                     160
```

Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
                165   170   175

Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
                180   185   190

Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
                195   200   205

Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
                210   215   220

Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225   230   235   240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
                245   250   255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
                260   265   270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
                275   280   285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
                290   295   300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305   310   315   320

Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
            325   330   335

Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
            340   345   350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
            355   360   365

Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu
            370   375   380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385   390   395   400

Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
            405   410   415

Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
            420   425   430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
            435   440   445

Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
450   455   460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu

```
      465                   470                   475                   480


Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
                    485                   490                   495


Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
                    500                   505                   510


Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
                    515                   520                   525


Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
          530                   535                   540


Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545                   550                   555                   560


Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
                    565                   570                   575


Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
                    580                   585                   590


Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
                    595                   600                   605


Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
          610                   615                   620
```

Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625   630   635   640

Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
                645   650   655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
                660   665   670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
                675   680   685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
                690   695   700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705   710   715   720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
                725   730   735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
                740   745   750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
                755   760   765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
                770   775   780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg

785   790   795   800

Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser

          805   810   815

Asp Arg Leu Arg Ile Ser Glu Lys

        820

<210> 132

<211> 2828

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (165)..(2636)

<400> 132

ggggcggggа gcggacttcc tcctctgagg gccgtgccgc gctgccagat ttgttcttcc 60

gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtgacg 120

gggcgggcgg gagccccggc agtccggggt cgccggcgag ggcc atg tcg ctg ttg 176

                                                     Met Ser Leu Leu

                                                        1

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ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg      224
Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro
 5                  10                  15                  20


ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg      272
Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro
                    25                  30                  35


ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg      320
Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg
                40                  45                  50


ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc      368
Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg
            55                  60                  65


ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct      416
Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro
            70                  75                  80


gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt      464
Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly
 85                  90                  95                  100


tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act      512
Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr
                    105                 110                 115


gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac      560
```

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn
        120   125   130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc   608
Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys
        135   140   145

cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat   656
Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn
        150   155   160

aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg   704
Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val
150   170   175   180

cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc   752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe
             185   190   195

acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca   800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro
        200   205   210

gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa   848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln
        215   220   225

atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg   896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu

```
        230                    235                    240

gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg    944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp
245                    250                    255                    260


ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg    992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met
                       265                    270                    275


gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta   1040
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val
                       280                    285                    290


tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata   1088
Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile
                       295                    300                    305


gga aga aca gat gag gca gtg gag tgc act gaa gat gaa tta aat aat   1136
Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu Asn Asn
310                    315                    320


ctt ggt cat cct gat aat aaa gag caa aca act gac cag cct ttg gcg   1184
Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala
325                    330                    335                    340


aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac   1232
Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg Glu His
                       345                    350                    355
```

```
ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta    1280
Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr Asn Leu
            360                 365                 370

ctg aga cag ctg gac ttc aaa gtg gtt tca ctg ttg gat ctt act gaa    1328
Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu Thr Glu
            375                 380                 385

tat gag atg cgt aat gct gtg gat gag ttt tta ctc ctt tta gac aag    1376
Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Asp Lys
            390               395                 400

gga gta tat ggg tta tta tat tat gca gga cat ggt tat gaa aat ttt    1424
Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu Asn Phe
405             410                 415                 420

ggg aac agc ttc atg gtc ccc gtt gat gct cca aat cca tat agg tct    1472
Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr Arg Ser
                425                 430                 435

gaa aat tgt ctg tgt gta caa aat ata ctg aaa ttg atg caa gaa aaa    1520
Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln Glu Lys
                440                 445                 450

gaa act gga ctt aat gtg ttc tta ttg gat atg tgt agg aaa aga aat    1568
Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys Arg Asn
                455                 460                 465
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537   出証特2002-3032935

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gac tac gat gat acc att cca atc ttg gat gca cta aaa gtc acc gcc    1616
Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala
    470             475                 480


aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa    1664
Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu
485             490                 495                 500


atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa    1712
Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys
                505                 510                 515


gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt    1760
Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp Glu Val
            520                 525                 530


gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta    1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
        535                 540                 545


gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata    1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
    550                 555                 560


cag gga aca gaa tat tct gct gaa tct ctt gtg cgg aat cta cag tgg    1904
Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
565                 570                 575                 580


gcc aag gct cat gaa ctt cca gaa agt atg tgt ctt aag ttt gac tgt    1952
```

Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe Asp Cys
         585   590   595

ggt gtt cag att caa tta gga ttt gca gct gag ttt tcc aat gtc atg   2000
Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn Val Met
         600   605   610

atc atc tat aca agt ata gtt tac aaa cca ccg gag ata ata atg tgt   2048
Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
         615   620   625

gat gcc tac gtt act gat ttt cca ctt gat cta gat att gat cca aaa   2096
Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys
         630   635   640

gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca   2144
Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser
645   650   655   660

aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa   2192
Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln
         665   670   675

aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac   2240
Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr
         680   685   690

tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg   2288
Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly

```
          695                    700                    705

aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag   2336
Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly Arg Lys
      710                    715                    720

act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct   2384
Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln Ser Ser
725                    730                    735                    740

gca gcc acc tca gga gga gca ggg cat tat cac tca ttg caa gac cca   2432
Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro
                  745                    750                    755

ttc cat ggt gtt tac cat tca cat cct ggt aat cca agt aat gtt aca   2480
Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr
                  760                    765                    770

cca gca gat agc tgt cat tgc agc cgg act cca gat gca ttt att tca   2528
Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser
                  775                    780                    785

agt ttc gct cac cat gct tca tgt cat ttt agt aga agt aat gtg cca   2576
Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn Val Pro
      790                    795                    800

gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga   2624
Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg
805                    810                    815                    820
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att tct gaa aaa tgacctcctt gtttttgaaa gttagcataa ttttagatgc   2676
Ile Ser Glu Lys

ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

gtagagaaag aatagtagta actgtttcat agcaaacttc aggactttga gatgttgaaa 2796

ttacattatt taattacaga cttcctcttt ct   2828

<210> 133

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<213> Homo sapiens

<400> 133

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn Glu Thr
1   5   10   15

Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro Val Ser
            20   25   30

Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu Asn Lys
        35   40   45

Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp
    50   55   60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys
65   70   75   80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu
                85   90   95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile
                100   105   110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu
            115   120   125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu
            130   135   140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr
145   150   155   160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe
                165   170   175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr
                180   185   190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly
                195   200   205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg
                210   215   220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu
225   230   235   240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr
                    245   250   255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr
                    260   265   270

Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly
                    275   280   285

Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
                    290   295   300

Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
305   310   315   320

Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
                    325   330   335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
                    340   345   350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
                    355   360   365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly

370   375   380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385   390   395   400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
                405   410   415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
                420   425   430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
                435   440   445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
                450   455   460

Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
465   470   475   480

Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
                485   490   495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
                500   505   510

Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
                515   520   525

Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
   530   535   540

Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
530   550   555   560
545

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
         565   570   575

Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr Ser Gln
         580   585   590

Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln Leu Ser
         595   600   605

Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro Arg His
   610   615   620

Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val Val Ala
625   630   635   640

Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp
         645   650   655

Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys Glu Ala
         660   665   670

Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met Ser Ala
         675   680   685

Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe Val Arg
    690   695   700

Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser Leu Ala
705   710   715   720

Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp
           725   730   735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu
           740   745   750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp
       755   760   765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile
  770   775   780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp
785   790   795   800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val
          805   810   815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser
        820   825   830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

           835   840   845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu
    850   855   860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe
865   870   875   880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys
                   885   890   895

Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr
        900   905   910

Ser Ser Ser Phe Leu Glu Val
        915

<210> 134

<211> 3612

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (427)..(3183)

<400> 134

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cctccccgcc cgccctctct ccctcccttc ctccctcccg ctcgcttctt ctcacgccgg 120

gagcaggctc ccgcctcgca ccgctgcccc gcgagcagct cctcttctcc cgaggcgcgc 180

ggggcgcccc cgcgagcccc gcggctgaga ccccgcagcc tggaggaggg ctgtccgggg 240

ctttggatgc tgctgctagg ggtggtggga gcagccgtgg gacgcgtggc cgggagcggg 300

ggtgacagcc tgggattccg ggggcttctc ttccttgtcc tcctcctctc ctctctattc 360

ccagtgtggc cgtggctgac actaaagact ttgtagccat caacccgagt gcagtttcga 420

tggaaa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat   468
        Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn
        1   5   10

gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca   516
Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro
15   20   25   30

gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta   564
Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu
          35   40   45

aac aaa tgt gaa gtt agt cat agg cga gcc ttt cat ggc tgg aat gag   612
Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu
        50   55   60

ttt gat att agt gaa gat gag cca ctg tgg aag aag tat att tct cag   660
Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln
         65   70   75

ttt aaa aat ccc ctt att atg ctg ctt ctg gct tct gca gtc atc agt   708
Phe Lys Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser
         80   85   90

gtt tta atg cat cag ttt gat gat gcc gtc agt atc act gtg gca ata   756
Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile
95   100   105   110

ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa   804
Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys
              115   120   125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg   852
Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val
             130   135   140

cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt   900
Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly
             145   150   155

gat aca gtt tgc ctt tct gtt ggg gat aga gtt cct gct gac tta cgc   948
Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg
             160   165   170

ttg ttt gag gct gtg gat ctt tcc att gat gag tcc agc ttg aca ggt   996

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                 Leu Phe Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly
                 175             180             185             190


gag aca acg cct tgt tct aag gtg aca gct cct cag cca gct gca act       1044
Glu Thr Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr
                 195             200             205


aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg       1092
Asn Gly Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu
                 210             215             220


gtc aga tgt ggc aaa gca aag ggt gtt gtc att gga aca gga gaa aat       1140
Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn
                 225             230             235


tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca       1188
Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro
                 240             245             250


aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc       1236
Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser
255              260             265             270


ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta       1284
Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu
                 275             280             285


ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct       1332
Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala
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             290                    295                    300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta   1380
Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu
        305                    310                    315


gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag   1428
Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys
        320                    325                    330


ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat   1476
Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp
335                    340                    345                    350


aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt   1524
Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe
                    355                    360                    365


act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa   1572
Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln
                    370                    375                    380


ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac   1620
Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn
        385                    390                    395


cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct   1668
Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala
        400                    405                    410
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gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta    1716
Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu
415             420             425             430


att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac    1764
Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr
            435             440             445


atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct    1812
Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala
            450             455             460


gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt    1860
Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe
        465             470             475


atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag    1908
Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln
    480             485             490


agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac    1956
Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
495             500             505             510


caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct    2004
Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
        515             520             525
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ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg   2052
Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
            530   535   540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca   2100
Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
            545   550   555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag   2148
Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
            560   565   570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act   2196
Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
575   580   585   590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag   2244
Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
            595   600   605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca   2292
Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
            610   615   620

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt   2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val
            625   630   635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct   2388

Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala
          640   645   650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa   2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys
655   660   665   670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg   2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met
                    675   680   685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc   2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe
                690   695   700

gtt aga ttc cag ctg agc acg agt ata gca gca tta act tta atc tca   2580
Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser
          705   710   715

ttg gct aca tta atg aac ttt cct aat cct ctc aat gcc atg cag att   2628
Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile
          720   725   730

ttg tgg atc aat att att atg gat gga ccc cca gct cag agc ctt gga   2676
Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly
735   740   745   750

gta gaa cca gtg gat aaa gat gtc att cgt aaa cct cct cgc aac tgg   2724
Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp

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                755                   760                   765


aaa gac agc att ttg act aaa aac ttg ata ctt aaa ata ctt gtt tca   2772
Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser
            770                   775                   780


tca ata atc att gtt tgt ggg act ttg ttt gtc ttc tgg cgt gag cta   2820
Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu
            785                   790                   795


cga gac aat gtg att aca cct cga gac aca aca atg acc ttc aca tgc   2868
Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys
        800                   805                   810


ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc   2916
Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr
815                   820                   825                   830


aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat   2964
Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr
                835                   840                   845


gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct   3012
Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro
            850                   855                   860


ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg   3060
Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu
            865                   870                   875
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ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att    3108
Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile
    880                 885                 890


ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt    3156
Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser
895                 900                 905                 910


tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt    3203
Ser Thr Ser Ser Ser Phe Leu Glu Val
                915


tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263


tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323


ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383


ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443


aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503


cactatctat cttagataga tatatttttt tttattttta aatattgtac tatttatggt 3563


ggtggggctt tcttactaat acacaaataa atttaatcat ttcaaaggc         3612
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<210> 135

<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

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Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln
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Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp
                20                  25                  30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser
            35                  40                  45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly
            50                  55                  60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr
65                  70                  75                  80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn
                    85                  90                  95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met
                100                 105                 110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr
                115                 120                 125
```

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys
    130   135   140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe
145   150   155   160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln
            165   170   175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala
            180   185   190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys
            195   200   205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile
210   215   220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly
225   230   235   240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser
            245   250   255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val
            260   265   270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu
            275   280   285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys
　　290　　　　　　　　295　　　　　　　　300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile
305　　　　　　　　310　　　　　　　　315　　　　　　　　320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr
　　　　　　　325　　　　　　　　330　　　　　　　　335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala
　　　　　340　　　　　　　　345　　　　　　　　350

Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr
　　　355　　　　　　　　360　　　　　　　　365

Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp
　　370　　　　　　　375　　　　　　　　380

<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (444)..(1589)

<400> 136

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cgggtcctca ggcggctgtt gctccggaac gggtggttgg ggaggggggg gtggggggac 120


tctagacagc tgaggcgcga aagcgatgag tcctcggctc ttcctcctcc ttctccggga 180


cccgctctct gcctccctct ccaacgcccg gatgatctga gccgcgaggg cgccgacagc 240


cgggggcccg gacgcagccc ggctcctccc ctcctccgcc ccttccccag cctgacctgg 300


cccgccgctg cagcggtgac ccctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360


tccccggctg ccgccgccgc cgcctcggcc gaccagggac ctgcccgcct gcggctgctc 420


cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473
                             Met Gly Ala Phe Leu Asp Lys Pro Lys Met
                             1               5                  10


gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta   521
Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu
                15                  20                  25


agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct   569
Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala
            30                  35                  40


gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg   617
Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val
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              45                    50                    55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat    665
Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His
         60                    65                    70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga    713
Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly
    75                    80                    85                    90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg    761
Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu
                   95                   100                   105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca    809
Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala
              110                   115                   120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat    857
Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His
         125                   130                   135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac    905
Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn
    140                   145                   150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg    953
Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu
155                   160                   165                   170
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```
gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt    1001
Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg
              175             180             185


gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac    1049
Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr
              190             195             200


aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag    1097
Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu
              205             210             215


cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att    1145
Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile
              220             225             230


atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc    1193
Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu
235             240             245             250


tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa    1241
Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys
              255             260             265


gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac    1289
Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp
              270             275             280
```

```
aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg    1337
Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser
        285                 290                 295


cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc    1385
Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys
        300                 305                 310


aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta    1433
Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu
315                 320                 325                 330


gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca    1481
Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro
                335                 340                 345


cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac    1529
Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr
                350                 355                 360


aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca    1577
Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr
                365                 370                 375


gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc        1629
Asp Asp Met Trp
        380


aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatcctcaa ctttaaggaa  1689
```

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtac aacagctagc 1749

ccagaactga tttttttttt tttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaat cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaat tatgaactgc tttaaatcac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatata tagccctttc 1989

aagtcatgtt gtgtttggac ttggggttgg aacagggaga gcagcagcca tgtcagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaatgt tcttggtagg ggagttggca ttgttgataa 2169

agccagtccc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtaataa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtcc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val
1   5   ·10   15

Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp
                20   25   30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu
                35   40   45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
        50   55   60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
65   70   75   80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn
                    85   90   95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
                100   105   110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
                115   120   125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
　　　 130　　　　　　　　 135　　　　　　　　 140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
145　　　　　　　　 150　　　　　　　　 155　　　　　　　　 160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
　　　　　　　　　 165　　　　　　　　 170　　　　　　　　 175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
　　　　　　　　 180　　　　　　　 185　　　　　　　　 190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln
　　　　　　　　 195　　　　　　　　 200　　　　　　　　 205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln
　　　　 210　　　　　　　　 215　　　　　　　　 220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro
225　　　　　　　　 230　　　　　　　　 235　　　　　　　　 240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln
　　　　　　　　 245　　　　　　　　 250　　　　　　　　 255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln
　　　　　　　　 260　　　　　　　　 265　　　　　　　　 270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr
　　　　　　　 275　　　　　　　　 280　　　　　　　　 285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln
        290   295   300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly
305   310   315   320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro
                325   330   335

Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln
                340   345   350

Pro Gly Pro Gly Tyr Arg
        355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

attagtgcta atg atg caa cga gtt ttc aga gga aaa ctt ctg agt aat   49
          Met Met Gln Arg Val Phe Arg Gly Lys Leu Leu Ser Asn

```
         1                    5                    10

gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca   97
Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr
        15                   20                   25


att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata   145
Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile
        30                   35                   40                   45


ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca   193
Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser
                 50                   55                   60


agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa   241
Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys
                 65                   70                   75


gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct   289
Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro
                 80                   85                   90


tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag   337
Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys
        95                   100                  105


tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca   385
Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala
110                  115                  120                  125
```

```
agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa    433
Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys
            130                 135                 140


aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca    481
Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro
            145                 150                 155


ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct    529
Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala
            160                 165                 170


tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca    577
Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
            175                 180                 185


cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac    625
Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
190                 195                 200                 205


cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag    673
Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
            210                 215                 220


cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag    721
Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
            225                 230                 235
```

```
act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca     769
Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
        240             245             250


act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg     817
Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
        255             260             265


cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa     865
Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
270             275             280             285


act tac act gcc caa act tct cag cct act aat tat act gtg gct cct     913
Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
            290             295             300


gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca     961
Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
            305             310             315


aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca    1009
Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
            320             325             330


agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc    1057
Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
            335             340             345


tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc          1104
Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
```

Tyr Thr Gln Pro Gly Pro Gly Tyr Arg

350   355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatatcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tccctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtgattga 1344

cttgactttc tagcttccct tgtccggagg atattaaaat gctagggtga ggtttagcca 1404

tcttacttgg cttttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc   1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1   5   10   15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20   25   30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu
            35   40   45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp
            50   55   60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys
    65   70   75   80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro
                85   90   95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
                100   105   110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
            115   120   125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
            130   135   140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145   150   155   160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
                165   170   175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val

```
                180                     185                     190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
            195                     200                     205


Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
            210                     215                     220


Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225                     230                     235                     240


Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
                        245                     250                     255


Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
                260                     265                     270


Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
                275                     280                     285


Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
            290                     295                     300


Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305                     310                     315                     320


Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
                        325                     330                     335
```

```
Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
            340                 345                 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
            355                 360                 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
            370                 375                 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385                 390                 395
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<210> 140

<211> 1641

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (19)..(1206)

<400> 140

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aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta     51
                    Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
                     1                   5                  10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat     99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
```

```
                15                    20                    25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt    147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
            30                    35                    40


ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa    195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
        45                    50                    55


gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc    243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
    60                    65                    70                    75


ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat    291
Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn
                80                    85                    90


ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga    339
Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg
            95                    100                    105


gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg    387
Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu
        110                    115                    120


gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat    435
Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp
        125                    130                    135
```

```
act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa      483
Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys
140             145             150             155


cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta      531
Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu
                160             165             170


aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta      579
Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu
                175             180             185


aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt      627
Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg
            190             195             200


tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca      675
Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro
            205             210             215


cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa      723
Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln
220             225             230             235


gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca      771
Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala
            240             245             250
```

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819
Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln
        255   260   265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867
Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln
        270   275   280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915
Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala
        285   290   295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963
Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
300   305   310   315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
                320   325   330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
                335   340   345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
                350   355   360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155

出証特2002-3032935

Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
   365   370   375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat   1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
380   385   390   395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc   1256
Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag   1316

cattttttat gatatcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga   1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga   1436

acactactct tacatgtata aagtgattga cttgactttc tagcttccct tgtccggagg   1496

atattaaaat gctagggtga ggtttagcca tcttacttgg ctttttacta ttaacatgat   1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga   1616

taggttaata aagatgattg aatcc   1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

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Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro
1               5              10              15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr
                20              25              30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn
                35              40              45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro
        50              55              60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65              70              75              80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
                85              90              95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
                100             105             110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
                115             120             125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
                130             135             140
```

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145   150   155   160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
                  165   170   175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
                  180   185   190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
              195   200   205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile
          210   215   220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe
225   230   235   240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly
                  245   250   255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln
                  260   265   270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala
              275   280   285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu
              290   295   300

```
Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His
305             310             315             320


Val Gln Thr
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<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

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aagtcgttcc ctctacaaag gacttcctag tgggtgtgaa aggcagcggt ggccacagag 60


gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca  110
            Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro
              1               5                  10


gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt  158
Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu
        15              20              25


cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt  206
```

```
Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe
30              35              40              45


gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac    254
Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His
                50              55              60


ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg    302
Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg
            65              70              75


cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc    350
Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe
        80              85              90


cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat    398
Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp
        95              100             105


ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc    446
Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg
110             115             120             125


gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag    494
Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln
                130             135             140


ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg    542
Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro
```

```
                 145                    150                         155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga    590
Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly
         160                    165                    170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc    638
Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro
         175                    180                    185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca    686
Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro
190                    195                    200                    205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg    734
Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg
                 210                    215                    220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac    782
Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn
                 225                    230                    235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac    830
Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn
         240                    245                    250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc    878
Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val
         255                    260                    265
```

```
cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc    926
Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu
270             275             280             285


aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg    974
Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu
                290             295             300


agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag   1022
Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln
                    305             310             315


ctg acc cat gtg cag aca taggcggctt cctggccctg gggccggggg         1070
Leu Thr His Val Gln Thr
                    320


ctggggtgtg gggcagtctg ggtcctctca tcatccccac ttcccaggcc cagcctttcc 1130


aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tcctgcttct 1190


ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250


cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310


agaggggagg agtgggcagt gaagatgaag ccccatgctc agtcccctcc catcccccac 1370


gcagctccac cccagtccca agccaccagc tgtctgctcc tggtgggagg tggcctcctc 1430
```

agcccctcct ctctgacctt taacctcact ctcaccttgc accgtgcacc aacccttcac 1490

ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc tttcccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile
1   5   10   15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly
                20   25   30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val
                35   40   45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val
        50   55   60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala
65   70   75   80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile
          85   90   95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His
         100   105   110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe
         115   120   125

Leu Gln Pro Leu Met His Cys Val
         130   135

<210> 144

<211> 1252

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (225)..(632)

<400> 144

acaatcacag ctccgggcat tgggggaacc cgagccggct gcgccggggg aatccgtgcg 60

ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggcgc aaaa atg gct ggg gca   236
                                                  Met Ala Gly Ala
                                                  1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att   284
Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
5   10   15   20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct   332
Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
              25   30   35

cca ggg ccc aca acg gca gtg tcc tac atg tcg gtg aaa tgt gtg gat   380
Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp
              40   45   50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc   428
Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro
              55   60   65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa   476
Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu
           70   75   80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac   524
Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His
85   90   95   100

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atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca    572
Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser
                105             110             115


gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta    620
Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu
                120             125             130


atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca        672
Met His Cys Val
                135


ttgttaatta gtgacatagt aacatctgta gcagctggtt agtaaacctc atgtggggggt  732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac  792

attttttcctg ttttaaattc taggatagat tttaacatcc tttgcggtcc cagtccaagg  852

taggctggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat  912

atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tccctgtttt  972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212
```

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc   1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
1   5   10   15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe
            20   25   30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln
            35   40   45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg
        50   55   60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro
65   70   75   80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu
                85   90   95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser

```
                 100                    105                      110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu
         115                  120                  125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu
         130                  135                  140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met
145                  150                  155                  160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp
                 165                  170                  175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
             180                  185                  190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
                 195                  200                  205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
         210                  215                  220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225                  230                  235                  240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
                 245                  250                  255
```

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
        260   265   270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
        275   280   285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
        290   295   300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305   310   315   320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser
        325   330   335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile
        340   345   350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met
        355   360   365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys
        370   375   380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile
385   390   395   400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala
        405   410   415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu
            420   425   430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr
            435   440   445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala
            450   455   460

Ala Ser Gly Ile
465

<210> 146

<211> 1943

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (379)..(1782)

<400> 146

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ggcgccttcc gtcccggtcc catcctcgcc gcgctccagc acctctgaag ttttgcagcg 120

cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcaccct 180

aaaacattta tttcaaggag aaaagaaaaa ggggggggcgc aaaaatggct ggggcaatta 240

tagaaaacat gagcaccaag aagctgtgca ttgttggtgg gattctgctc gtgttccaaa 300

tcatcgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360

tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt   411
                          Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
                          1   5   10

tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag   459
Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys
              15   20   25

agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc   507
Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe
          30   35   40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt   555
Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val
          45   50   55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc   603
Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala
60   65   70   75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag   651
His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

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                80                  85                  90


act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc   699
Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe
            95                  100                 105


atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg   747
Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg
            110                 115                 120


ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata   795
Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile
        125                 130                 135


aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag   843
Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys
140                 145                 150                 155


gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att   891
Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile
                160                 165                 170


atg gtg tgg tat tgg agg agg atc acc atg atg tcc cga ccc cca gtg   939
Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val
                175                 180                 185


ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc   987
Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile
            190                 195                 200
```

```
aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg      1035
Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met
    205                 210                 215


ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg      1083
Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu
220                 225                 230                 235


tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag      1131
Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu
                240                 245                 250


cgg aac cac atc gca ggg tat tgg aag caa gtc gga ccc att gcc gtt      1179
Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val
                255                 260                 265


ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa      1227
Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln
                270                 275                 280


ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag      1275
Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu
                285                 290                 295


ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac      1323
Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr
300                 305                 310                 315
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ttc ctg ttt cta tgc ttc atg gta ttt cag gtg ttt cgg aac atc agt    1371
Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser
              320               325               330


ggg aag cag tcc agc ctg cca gct atg agc aaa gtc cgg cgg cta cac    1419
Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg Arg Leu His
              335               340               345


tat gag ggg cta att ttt agg ttc aag ttc ctc atg ctt atc acc ttg    1467
Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu
              350               355               360


gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg    1515
Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr
              365               370               375


gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc    1563
Glu Gly His Trp Lys Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala
380               385               390               395


ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg    1611
Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu
              400               405               410


atg ttc ttg tat gca cca tcc cat aaa aac tat gga gaa gac cag tcc    1659
Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser
              415               420               425


aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt    1707
```

Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe
        430   435   440

gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc   1755
Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe
        445   450   455

atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca   1802
Ile Asn Asp Asn Ala Ala Ser Gly Ile
460   465

tgtttatcag ctttgcattt gcagttgtca cagtcacatt gattgtactt gtatacgcac 1862

acaaatacac tcatttagcc tttatctcaa aatgttaaat ataaggaaaa aagcgtcaac 1922

aataaatatt ctttgagtat t   1943

<210> 147

<211> 460

<212> PRT

<213> Homo sapiens

<400> 147

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp
 1   5   10   15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Gly
        20   25   30

出証特２００２−３０３２９３５

Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr Phe Pro Ser Pro
         35   40   45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr
         50   55   60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr
         65   70   75   80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val
                 85   90   95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
             100   105   110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
           115   120   125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
        130   135   140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
145   150   155   160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
           165   170   175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met

```
                     180                       185                          190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
            195                       200                       205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
       210                    215                    220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
   225                    230                    235                    240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
                    245                    250                    255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg
                260                    265                    270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile
            275                    280                    285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu
       290                    295                    300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg
305                    310                    315                    320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg
                325                    330                    335
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Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu
      340   345   350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser
      355   360   365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val
      370   375   380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val
385   390   395   400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu
      405   410   415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys
      420   425   430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys
      435   440   445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
      450   455   460

<210> 148

<211> 1919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (376)..(1755)

<400> 148

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gccttccgtc ccggtcccat cctcgccgcg ctccagcacc tctgaagttt tgcagcgccc 120

agaaaggagg cgaggaagga gggagtgtat gagaggaggg agcaaaaagc tcaccctaaa 180

acatttattt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tcgcctttct ggtgggaggc ttgattgctc cagggcccac aacggcagtg tcctacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tcg 411
                Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser
                  1   5   10

tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459
Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg
        15   20   25

caa ttc caa ggg aaa ttg aag cca atg aca tcg tgt ttt ctg ttc aca 507
Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr
     30   35   40

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ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt    555
Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe
 45              50              55              60


gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa    603
Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys
                65              70              75


tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat    651
Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr
                80              85              90


gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag    699
Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
                95              100             105


ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc    747
Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
 110             115             120


aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac    795
Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
125             130             135             140


caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt    843
Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
                145             150             155
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```
acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc     891
Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
            160                 165                 170


atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt     939
Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
            175                 180                 185


ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc     987
Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
        190                 195                 200


ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc    1035
Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
205                 210                 215                 220


atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag    1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
                225                 230                 235


cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag    1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
            240                 245                 250


caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac    1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
            255                 260                 265


atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg    1227
```

```
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
    270             275             280
```

```
act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct    1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
285             290             295             300
```

```
gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt    1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
            305             310             315
```

```
cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg    1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met
            320             325             330
```

```
agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag    1419
Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys
            335             340             345
```

```
ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc    1467
Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe
    350             355             360
```

```
ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc    1515
Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile
365             370             375             380
```

```
aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg    1563
Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp
```

```
                385                   390                   395


aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa   1611
Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys
                400                   405                   410


aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg   1659
Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser
                415                   420                   425


agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc   1707
Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe
            430                   435                   440


agc gct tcg aaa tat tcc ttc atc aat gac aac gca gct tct ggt att   1755
Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile
445                   450                   455                   460


tgagtcaaca aggcaacaca tgtttatcag ctttgcattt gcagttgtca cagtcacatt   1815


gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaat   1875


ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc                     1919
```

<210> 149

<211> 183

<212> PRT

<213> Homo sapiens

<400> 149

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
1   5   10   15

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
                20   25   30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
                35   40   45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
            50   55   60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
65   70   75   80

Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                    85   90   95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
                100   105   110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
                115   120   125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
                130   135   140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145   150   155   160

Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                  165   170   175

Asp Arg His Lys Met Leu Ser
                  180

<210> 150

<211> 1562

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (120)..(668)

<400> 150

tacggctgcg agaagacgac agaaggggat taagagggag ggcggggaca actgggtctt 60

ttgcggctgc agcgggcttg taggtgtccg gctttgctgg cccagcaagc ctgataagc 119

atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro
 1   5   10   15

cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

```
                  Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile
                          20              25                  30


tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta   263
Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val
        35              40                  45


tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg   311
Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val
        50              55                  60


cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac   359
Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
  65              70                  75                  80


gag gag cgc agc acc acc acc atc aag gtc atc att gtc atc tac ctg   407
Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
                85                  90                  95


tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg   455
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
                100                 105                 110


gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat   503
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
                115                 120                 125


gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc   551
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser
```

```
        130                    135                    140

ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc   599
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145                    150                    155                    160


cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc   647
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe
                    165                    170                    175


gat cgg cac aag atg ctc agc tagatgggct ggtgtggttg ggtcaaggcc      698
Asp Arg His Lys Met Leu Ser
                180


ccaacaccat ggctgccagc ttccaggctg acaaagcag ggggctactt ctcccttccc   758

tcggttccag tcttcccttt aaaagcctgt ggcatttttc ctccttctcc ctaactttag   818

aaatgttgta cttggctatt ttgattaggg aagagggatg tggtctctga tctccgttgt   878

cttcttgggt ctttgggggtt gaagggaggg ggaaggcagg ccagaaggga atggagacat   938

tcgaggcggc ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc   998

cagctctgag tcttgggaat gttgttaccc ttggaagata aagctgggtc ttcaggaact  1058

cagtgtctgg gaggaaagca tggcccagca ttcagcatgt gttcctttct gcagtggttc  1118

tttatcacca cctccctccc agccccagcg cctcagcccc agccccagct ccagccctga  1178
```

ggacagctct gatgggagag ctgggcccccc tgagcccact gggtcttcag ggtgcactgg 1238

aagctggtgt tcgctgtccc ctgtgcactt ctcgcactgg ggcatggagt gcccatgcat 1298

actctgctgc cggtcccctc acctgcactt gaggggtctg ggcagtccct cctctcccca 1358

gtgtccacag tcactgagcc agacggtcgg ttggaacatg agactcgagg ctgagcgtgg 1418

atctgaacac cacagccct gtacttgggt tgcctcttgt ccctgaactt cgttgtacca 1478

gtgcatggag agaaaatttt gtcctcttgt cttagagttg tgtgtaaatc aaggaagcca 1538

tcattaaatt gttttatttc tctc   1562

<210> 151

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)..(2387)

<400> 151

tctctcctcc tcctccagca gccaccaggg accgggagat ctaccagctc aagacccta 60

cagccaggtc tgtgctgccg ccctccagca tctttgcagc aggggacgag gctgtgtggg 120

aggctgtcgg ttcggaacat gtctccaccc accccaccct ctgtggctcc aggcttcatt 180

ctcccccatc c atg gat aac cca ggg cct tcg ctc cgt ggt gcc ttt ggc 230
　　　　　　　Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly
　　　　　　　　1　　　　　　　　5　　　　　　　　　　10

att cta ggt gcc ttg gaa agg gac agg ctg acc cac ctg aaa cac aag 278
Ile Leu Gly Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys
　15　　　　　　　　20　　　　　　　　25

ctg ggg agt ctg tgt tca ggc agc cag gag tca aag ctt ctc cat gcc 326
Leu Gly Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala
　30　　　　　　　　35　　　　　　　　40　　　　　　　　45

atg gta ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg 374
Met Val Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu
　　　　　　　　50　　　　　　　　55　　　　　　　　60

gag tcc ttg aag atg aac aca gta gcc cag ctg gta gcc cac cag tgg 422
Glu Ser Leu Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp
　　　　　　　65　　　　　　　　70　　　　　　　　75

gca gac atg gag acc aca gag ggc cct gag gag cct cca gac ttg tcc 470
Ala Asp Met Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser
　　　　　　　80　　　　　　　　85　　　　　　　　90

tgg acg gtg gct cgc ctg tac cac ctg ctg gct gag gag aac ctg tgt 518
Trp Thr Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys

```
              95                  100                 105


ccg gcc tct aca agg gac atg gct tac cag gtg gcc ctt cgt gac ttt   566
Pro Ala Ser Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe
110                 115                 120                 125


gcc tcc cag ggt gac cac cag ctg ggc caa ctc cag aat gag gcc tgg   614
Ala Ser Gln Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp
                    130                 135                 140


gat cgg tgc agt tca gat atc aag ggg gac ccc agt ggt ttc cag cca   662
Asp Arg Cys Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro
                    145                 150                 155


ctc cat tct cat cag ggt tcc ctg cag cca cct tca gca tcc cct gca   710
Leu His Ser His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala
                    160                 165                 170


gtg acc aga agc cag cct cgt ccc att gac aca cca gac tgg agt tgg   758
Val Thr Arg Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp
                    175                 180                 185


gga cat acg tta cac tcc acc aac agc act gcc tca ctg gcc agc cac   806
Gly His Thr Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His
190                 195                 200                 205


cta gag atc agc cag tca ccc act ctt gcc ttt ctc tct tca cac cat   854
Leu Glu Ile Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His
                    210                 215                 220
```

```
gga acc cat ggg ccc agc aag cta tgt aac aca ccg ctg gac act cag    902
Gly Thr His Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln
            225             230             235


gag cct cag ctt gtc cct gaa ggc tgc caa gaa cct gag gag ata agc    950
Glu Pro Gln Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser
            240             245             250


tgg cct cca tca gtg gag acc agt gtc tcc tta ggg tta cca cac gaa    998
Trp Pro Pro Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu
            255             260             265


att agc gtt cca gag gtg tct cca gag gag gct tcg ccc atc ctc cct   1046
Ile Ser Val Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro
270             275             280             285


gac gcc ctg gct gct cca gac aca agt gtc cac tgt ccc att gaa tgc   1094
Asp Ala Leu Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys
            290             295             300


aca gag ttg tct aca aac tcc agg tct ccc ctg acg tcc acc aca gaa   1142
Thr Glu Leu Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu
            305             310             315


agt gtt gga aag cag tgg cct att aca agt cag agg tca cct cag gtt   1190
Ser Val Gly Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val
            320             325             330
```

cct gta gga gat gat tct ctg cag aac acc acg tca tcc agc cct cct   1238
Pro Val Gly Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro
    335   340   345

gcc cag cca cca tcc ctc caa gcc tcc cct aag ctg cct cct tcc cct   1286
Ala Gln Pro Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro
350   355   360   365

ctg tcc tct gct tcc tcc ccg agc agc tac cct gct cct cca acc tcc   1334
Leu Ser Ser Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser
                370   375   380

aca tcc cct gtt ttg gac cac tca gaa aca tct gat cag aaa ttc tat   1382
Thr Ser Pro Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr
                385   390   395

aac ttt gtg gtt atc cat gcc agg gct gat gaa cag gtg gcc cta cgt   1430
Asn Phe Val Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg
        400   405   410

att cgg gag aag ctg gag acc ctc ggg gta cct gac ggg gcc acc ttc   1478
Ile Arg Glu Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe
    415   420   425

tgt gag gaa ttt cag gtg ccc ggg cgt ggt gag ctg cac tgt ctc caa   1526
Cys Glu Glu Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln
430   435   440   445

gat gcc atc gat cac tcg ggg ttc acg atc ctg ctc ctg act gct agc   1574

Asp Ala Ile Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser
          450   455   460

ttt gat tgc agc ctg agc ctg cat caa atc aac cat gct ctc atg aac   1622
Phe Asp Cys Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn
          465   470   475

agc ctt aca cag tct ggg agg cag gac tgt gtg atc ccc ctc ctc cca   1670
Ser Leu Thr Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro
          480   485   490

ctt gag tgt tcc cag gcc cag ctc agc cca gat aca acc aga ctg ctc   1718
Leu Glu Cys Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu
          495   500   505

cac agc att gtg tgg ctg gat gaa cac tcc cca atc ttc gcc aga aag   1766
His Ser Ile Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys
510   515   520   525

gtg gca aac acc ttc aag aca cag aag ctc cag gca cag cgg gta cgc   1814
Val Ala Asn Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg
          530   535   540

tgg aag aaa gcg cag gag gcc aga acc ctc aag gag cag agc ata cag   1862
Trp Lys Lys Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln
          545   550   555

ctg gag gca gag cgg caa aac gtg gca gcc ata tct gct gcc tac aca   1910
Leu Glu Ala Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr

          出証特２００２－３０３２９３５

```
              560                   565                   570

gcc tat gtc cat agc tat agg gcc tgg caa gca gag atg aac aaa ctt    1958
Ala Tyr Val His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu
     575                   580                   585


ggg gtg gct ttt ggg aag aac ttg tca ctg ggg act cca aca ccc agc    2006
Gly Val Ala Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser
590                   595                   600                   605


tgg ccc gga tgt cca cag cca ata cct tct cat cct cag ggt ggt act    2054
Trp Pro Gly Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr
              610                   615                   620


cca gtt ttc ccc tat tcc cca cag cct cca tcc ttc cct cag cct cca    2102
Pro Val Phe Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro
              625                   630                   635


tgc ttc cct cag cct cca tcc ttc cct cag cct cca tcc ttc cca ctg    2150
Cys Phe Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu
              640                   645                   650


cct cca gtc tct tcc cca cag tcc caa tcc ttt cca tca gcc tcc tcc    2198
Pro Pro Val Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser
              655                   660                   665


cca gcc cca cag act cca gga cct cag cct ctc att att cac cat gcc    2246
Pro Ala Pro Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala
670                   675                   680                   685
```

```
cag atg gtt cag ctg ggt gtc aac aat cac atg tgg ggc cac aca ggg    2294
Gln Met Val Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly
            690                 695                 700


gcc cag tca tct gat gac aag act gag tgt tcg gag aac ccc tgt atg    2342
Ala Gln Ser Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met
            705                 710                 715


ggc cct ctg act gat cag ggc gaa ccc ctt ctt gag act cca gag        2387
Gly Pro Leu Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
            720                 725                 730


tgaccaggtt ggaccccacc tagatggcta gagtgacaag attggacttc acctgggtcc 2447

ttaaaatgat agtggaggaa gggaacctcg cctgggtccc cagagtagcc agaggactta 2507

gcttgggctc ccacagtggc tattagttgg acccagcttg agaccccaga ggcagggaag 2567

accacaccta taaatcaggc ctgggaaaca tgcagaaacc ccatttgaac agactgtggg 2627

actccaatct gaatcctcta tgtggacaga ggatgatggg gccagaggca cctctgaggt 2687

gccctcagcg cagcctcgta aacttcattc actgtgacac atgctgttca tagggtctct 2747

ctggggagga tgcggtcccg gggcacatag ggagggtcct gtttttataa taaagttatt 2807

gacaactg                                                           2815
```

<210> 152

<211> 732

<212> PRT

<213> Homo sapiens

<400> 152

Met Asp Asn Pro Gly Pro Ser Leu Arg Gly Ala Phe Gly Ile Leu Gly
1   5   10   15

Ala Leu Glu Arg Asp Arg Leu Thr His Leu Lys His Lys Leu Gly Ser
            20   25   30

Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val Leu
        35   40   45

Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser Leu
    50   55   60

Lys Met Asn Thr Val Ala Gln Leu Val Ala His Gln Trp Ala Asp Met
65   70   75   80

Glu Thr Thr Glu Gly Pro Glu Glu Pro Pro Asp Leu Ser Trp Thr Val
                85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Asn Leu Cys Pro Ala Ser
            100   105   110

Thr Arg Asp Met Ala Tyr Gln Val Ala Leu Arg Asp Phe Ala Ser Gln

```
            115                   120                   125

Gly Asp His Gln Leu Gly Gln Leu Gln Asn Glu Ala Trp Asp Arg Cys
            130                   135                   140

Ser Ser Asp Ile Lys Gly Asp Pro Ser Gly Phe Gln Pro Leu His Ser
145                   150                   155                   160

His Gln Gly Ser Leu Gln Pro Pro Ser Ala Ser Pro Ala Val Thr Arg
                      165                   170                   175

Ser Gln Pro Arg Pro Ile Asp Thr Pro Asp Trp Ser Trp Gly His Thr
                      180                   185                   190

Leu His Ser Thr Asn Ser Thr Ala Ser Leu Ala Ser His Leu Glu Ile
                      195                   200                   205

Ser Gln Ser Pro Thr Leu Ala Phe Leu Ser Ser His His Gly Thr His
            210                   215                   220

Gly Pro Ser Lys Leu Cys Asn Thr Pro Leu Asp Thr Gln Glu Pro Gln
225                   230                   235                   240

Leu Val Pro Glu Gly Cys Gln Glu Pro Glu Glu Ile Ser Trp Pro Pro
                      245                   250                   255

Ser Val Glu Thr Ser Val Ser Leu Gly Leu Pro His Glu Ile Ser Val
                      260                   265                   270
```

Pro Glu Val Ser Pro Glu Glu Ala Ser Pro Ile Leu Pro Asp Ala Leu
   275   280   285

Ala Ala Pro Asp Thr Ser Val His Cys Pro Ile Glu Cys Thr Glu Leu
   290   295   300

Ser Thr Asn Ser Arg Ser Pro Leu Thr Ser Thr Thr Glu Ser Val Gly
305   310   315   320

Lys Gln Trp Pro Ile Thr Ser Gln Arg Ser Pro Gln Val Pro Val Gly
     325   330   335

Asp Asp Ser Leu Gln Asn Thr Thr Ser Ser Ser Pro Pro Ala Gln Pro
     340   345   350

Pro Ser Leu Gln Ala Ser Pro Lys Leu Pro Pro Ser Pro Leu Ser Ser
     355   360   365

Ala Ser Ser Pro Ser Ser Tyr Pro Ala Pro Pro Thr Ser Thr Ser Pro
     370   375   380

Val Leu Asp His Ser Glu Thr Ser Asp Gln Lys Phe Tyr Asn Phe Val
385   390   395   400

Val Ile His Ala Arg Ala Asp Glu Gln Val Ala Leu Arg Ile Arg Glu
     405   410   415

Lys Leu Glu Thr Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Glu
     420   425   430

Phe Gln Val Pro Gly Arg Gly Glu Leu His Cys Leu Gln Asp Ala Ile
      435   440   445

Asp His Ser Gly Phe Thr Ile Leu Leu Leu Thr Ala Ser Phe Asp Cys
      450   455   460

Ser Leu Ser Leu His Gln Ile Asn His Ala Leu Met Asn Ser Leu Thr
465   470   475   480

Gln Ser Gly Arg Gln Asp Cys Val Ile Pro Leu Leu Pro Leu Glu Cys
              485   490   495

Ser Gln Ala Gln Leu Ser Pro Asp Thr Thr Arg Leu Leu His Ser Ile
      500   505   510

Val Trp Leu Asp Glu His Ser Pro Ile Phe Ala Arg Lys Val Ala Asn
      515   520   525

Thr Phe Lys Thr Gln Lys Leu Gln Ala Gln Arg Val Arg Trp Lys Lys
      530   535   540

Ala Gln Glu Ala Arg Thr Leu Lys Glu Gln Ser Ile Gln Leu Glu Ala
545   550   555   560

Glu Arg Gln Asn Val Ala Ala Ile Ser Ala Ala Tyr Thr Ala Tyr Val
              565   570   575

His Ser Tyr Arg Ala Trp Gln Ala Glu Met Asn Lys Leu Gly Val Ala

                580   585   590

Phe Gly Lys Asn Leu Ser Leu Gly Thr Pro Thr Pro Ser Trp Pro Gly
         595   600   605

Cys Pro Gln Pro Ile Pro Ser His Pro Gln Gly Gly Thr Pro Val Phe
         610   615   620

Pro Tyr Ser Pro Gln Pro Pro Ser Phe Pro Gln Pro Pro Cys Phe Pro
625   630   635   640

Gln Pro Pro Ser Phe Pro Gln Pro Pro Ser Phe Pro Leu Pro Pro Val
                   645   650   655

Ser Ser Pro Gln Ser Gln Ser Phe Pro Ser Ala Ser Ser Pro Ala Pro
                   660   665   670

Gln Thr Pro Gly Pro Gln Pro Leu Ile Ile His His Ala Gln Met Val
              675   680   685

Gln Leu Gly Val Asn Asn His Met Trp Gly His Thr Gly Ala Gln Ser
         690   695   700

Ser Asp Asp Lys Thr Glu Cys Ser Glu Asn Pro Cys Met Gly Pro Leu
705   710   715   720

Thr Asp Gln Gly Glu Pro Leu Leu Glu Thr Pro Glu
              725   730

<210> 153

<211> 2544

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (97)..(2232)

<400> 153

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tagggggacac tgggcgtgca gaaggcgggg ggcagtgtgg aacatgcctt caccacctcc   60


agcttctgct gccggaggct gcacccacct gtgccc atg gcc tgc aca ggc cca      114
                                          Met Ala Cys Thr Gly Pro
                                          1               5


tca ctt cct agc gcc ttc gac att cta ggt gca gca ggc cag gac aag     162
Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly Ala Ala Gly Gln Asp Lys
            10              15                  20


ctc ttg tat ctg aag cac aaa ctg aag acc cca cgc cca ggc tgc cag     210
Leu Leu Tyr Leu Lys His Lys Leu Lys Thr Pro Arg Pro Gly Cys Gln
            25              30                  35


ggg cag gac ctc ctg cat gcc atg gtt ctc ctg aag ctg ggc cag gaa     258
Gly Gln Asp Leu Leu His Ala Met Val Leu Leu Lys Leu Gly Gln Glu
        40              45                  50
```

```
act gag gcc agg atc tct cta gag gca ttg aag gcc gat gcg gtg gcc    306
Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu Lys Ala Asp Ala Val Ala
55                  60              65                  70


cgg ctg gtg gcc cgc cag tgg gct ggc gtg gac agc acc gag gac cca    354
Arg Leu Val Ala Arg Gln Trp Ala Gly Val Asp Ser Thr Glu Asp Pro
                75              80              85


gag gag ccc cca gat gtg tcc tgg gct gtg gcc cgc ttg tac cac ctg    402
Glu Glu Pro Pro Asp Val Ser Trp Ala Val Ala Arg Leu Tyr His Leu
            90              95              100


ctg gct gag gag aag ctg tgc ccc gcc tcg ctg cgg gac gtg gcc tac    450
Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser Leu Arg Asp Val Ala Tyr
            105             110             115


cag gaa gcc gtc cgc acc ctc agc tcc agg gac gac cac cgg ctg ggg    498
Gln Glu Ala Val Arg Thr Leu Ser Ser Arg Asp Asp His Arg Leu Gly
            120             125             130


gaa ctt cag gat gag gcc cga aac cgg tgt ggg tgg gac att gct ggg    546
Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys Gly Trp Asp Ile Ala Gly
135             140             145             150


gat cca ggg agc atc cgg acg ctc cag tcc aat ctg ggc tgc ctc cca    594
Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser Asn Leu Gly Cys Leu Pro
            155             160             165
```

出証特２００２−３０３２９３５

cca tcc tcg gct ttg ccc tct ggg acc agg agc ctc cca cgc ccc att 642
Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg Ser Leu Pro Arg Pro Ile
     170   175   180

gac ggt gtt tcg gac tgg agc caa ggg tgc tcc ctg cga tcc act ggc 690
Asp Gly Val Ser Asp Trp Ser Gln Gly Cys Ser Leu Arg Ser Thr Gly
     185   190   195

agc cct gcc tcc ctg gcc agc aac ttg gaa atc agc cag tcc cct acc 738
Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu Ile Ser Gln Ser Pro Thr
     200   205   210

atg ccc ttc ctc agc ctg cac cgc agc cca cat ggg ccc agc aag ctc 786
Met Pro Phe Leu Ser Leu His Arg Ser Pro His Gly Pro Ser Lys Leu
215   220   225   230

tgt gac gac ccc cag gcc agc ttg gtg ccc gag cct gtc ccc ggt ggc 834
Cys Asp Asp Pro Gln Ala Ser Leu Val Pro Glu Pro Val Pro Gly Gly
     235   240   245

tgc cag gag cct gag gag atg agc tgg ccg cca tcg ggg gag att gcc 882
Cys Gln Glu Pro Glu Glu Met Ser Trp Pro Pro Ser Gly Glu Ile Ala
     250   255   260

agc cca cca gag ctg cca agc agc cca cct cct ggg ctt ccc gaa gtg 930
Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro Pro Gly Leu Pro Glu Val
     265   270   275

gcc cca gat gca acc tcc act ggc ctc cct gat acc ccc gca gct cca 978

```
        Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro Asp Thr Pro Ala Ala Pro
            280             285             290


        gaa acc agc acc aac tac cca gtg gag tgc acc gag ggg tct gca ggc    1026
        Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys Thr Glu Gly Ser Ala Gly
        295             300             305             310


        ccc cag tct ctc ccc ttg cct att ctg gag ccg gtc aaa aac ccc tgc    1074
        Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu Pro Val Lys Asn Pro Cys
                        315             320             325


        tct gtc aaa gac cag acg cca ctc caa ctt tct gta gaa gat acc acc    1122
        Ser Val Lys Asp Gln Thr Pro Leu Gln Leu Ser Val Glu Asp Thr Thr
                    330             335             340


        tct cca aat acc aag ccg tgc cca cct act ccc acc acc cca gaa aca    1170
        Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr Pro Thr Thr Pro Glu Thr
                    345             350             355


        tcc cct cct cct cct cct cct cct cct tca tct act cct tgt tca gct    1218
        Ser Pro Pro Pro Pro Pro Pro Pro Ser Ser Thr Pro Cys Ser Ala
            360             365             370


        cac ctg acc ccc tcc tcc ctg ttc cct tcc tcc ctg gaa tca tca tcg    1266
        His Leu Thr Pro Ser Ser Leu Phe Pro Ser Ser Leu Glu Ser Ser Ser
        375             380             385             390


        gaa cag aaa ttc tat aac ttt gtg atc ctc cac gcc agg gca gac gaa    1314
        Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu His Ala Arg Ala Asp Glu
```

```
                395                    400                    405


cac atc gcc ctg cgg gtt cgg gag aag ctg gag gcc ctt ggc gtg ccc   1362
His Ile Ala Leu Arg Val Arg Glu Lys Leu Glu Ala Leu Gly Val Pro
        410                    415                    420


gac ggg gcc acc ttc tgc gag gat ttc cag gtg ccg ggg cgc ggg gag   1410
Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln Val Pro Gly Arg Gly Glu
        425                    430                    435


ctg agc tgc ctg cag gac gcc ata gac cac tca gct ttc atc atc cta   1458
Leu Ser Cys Leu Gln Asp Ala Ile Asp His Ser Ala Phe Ile Ile Leu
        440                    445                    450


ctt ctc acc tcc aac ttc gac tgt cgc ctg agc ctg cac cag gtg aac   1506
Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu Ser Leu His Gln Val Asn
455                    460                    465                    470


caa gcc atg atg agc aac ctc acg cga cag ggg tcg cca gac tgt gtc   1554
Gln Ala Met Met Ser Asn Leu Thr Arg Gln Gly Ser Pro Asp Cys Val
                475                    480                    485


atc ccc ttc ctg ccc ctg gag agc tcc ccg gcc cag ctc agc tcc gac   1602
Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro Ala Gln Leu Ser Ser Asp
        490                    495                    500


acg gcc agc ctg ctc tcc ggg ctg gtg cgg ctg gac gaa cac tcc cag   1650
Thr Ala Ser Leu Leu Ser Gly Leu Val Arg Leu Asp Glu His Ser Gln
        505                    510                    515
```

atc ttc gcc agg aag gtg gcc aac acc ttc aag ccc cac agg ctt cag   1698
Ile Phe Ala Arg Lys Val Ala Asn Thr Phe Lys Pro His Arg Leu Gln
  520   525   530

gcc cga aag gcc atg tgg agg aag gaa cag gac acc cga gcc ctg cgg   1746
Ala Arg Lys Ala Met Trp Arg Lys Glu Gln Asp Thr Arg Ala Leu Arg
535   540   545   550

gaa cag agc caa cac ctg gac ggt gag cgg atg cag gcg gcg gca ctg   1794
Glu Gln Ser Gln His Leu Asp Gly Glu Arg Met Gln Ala Ala Ala Leu
        555   560   565

aac gca gcc tac tca gcc tac ctc cag agc tac ttg tcc tac cag gca   1842
Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser Tyr Leu Ser Tyr Gln Ala
      570   575   580

cag atg gag cag ctc cag gtg gct ttt ggg agc cac atg tca ttt ggg   1890
Gln Met Glu Gln Leu Gln Val Ala Phe Gly Ser His Met Ser Phe Gly
      585   590   595

act ggg gcg ccc tat ggg gct cga atg ccc ttt ggg ggc cag gtg ccc   1938
Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro Phe Gly Gly Gln Val Pro
      600   605   610

ctg gga gcc ccg cca ccc ttt ccc act tgg ccg ggg tgc ccg cag ccg   1986
Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp Pro Gly Cys Pro Gln Pro
615   620   625   630

cca ccc ctg cac gca tgg cag gct ggc acc ccc cca ccg ccc tcc cca   2034
Pro Pro Leu His Ala Trp Gln Ala Gly Thr Pro Pro Pro Ser Pro
             635   640   645

cag cca gca gcc ttt cca cag tca ctg ccc ttc ccg cag tcc cca gcc   2082
Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro Phe Pro Gln Ser Pro Ala
             650   655   660

ttc cct acg gcc tca ccc gca ccc cct cag agc cca ggg ctg caa ccc   2130
Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln Ser Pro Gly Leu Gln Pro
             665   670   675

ctc att atc cac cac gca cag atg gta cag ctg ggg ctg aac aac cac   2178
Leu Ile Ile His His Ala Gln Met Val Gln Leu Gly Leu Asn Asn His
             680   685   690

atg tgg aac cag aga ggg tcc cag gcg ccc gag gac aag acg cag gag   2226
Met Trp Asn Gln Arg Gly Ser Gln Ala Pro Glu Asp Lys Thr Gln Glu
695   700   705   710

gca gaa tgaccgcgtg tccttgcctg accacctggg gaacacccct ggacccaggc   2282
Ala Glu

atcggccagg accccataga gcaccccggt ctgccctgtg ccctgtggac agtggaagat 2342

gaggtcatct gccactttca ggacattgtc cgggagccct tcatttagga caaaacgggc 2402

gcgatgatgc cctggctttc agggtggtca gaactggata cggtgtttac aattccaatc 2462

tctctatttc tgggtgaagg gtcttggtgg tggggggtatt gctacggtct tttaattata 2522

ataaatattt attgaatgct tc 2544

<210> 154

<211> 712

<212> PRT

<213> Homo sapiens

<400> 154

Met Ala Cys Thr Gly Pro Ser Leu Pro Ser Ala Phe Asp Ile Leu Gly
1   5   10   15

Ala Ala Gly Gln Asp Lys Leu Leu Tyr Leu Lys His Lys Leu Lys Thr
                20   25   30

Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
            35   40   45

Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala Leu
        50   55   60

Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
65   70   75   80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
                85   90   95

Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
                100   105   110

Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser Arg
            115   120   125

Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
        130   135   140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145   150   155   160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
                165   170   175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
                180   185   190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
                195   200   205

Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
        210   215   220

His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225   230   235   240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
                245   250   255

Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro Pro
          260   265   270

Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
          275   280   285

Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
          290   295   300

Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
305   310   315   320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
          325   330   335

Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
          340   345   350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser
          355   360   365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
          370   375   380

Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
385   390   395   400

His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu

```
                405                      410                      415

Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
            420                      425                      430

Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
            435                      440                      445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
            450                      455                      460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465                      470                      475                      480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
                485                      490                      495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
            500                      505                      510

Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
            515                      520                      525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
            530                      535                      540

Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
545                      550                      555                      560
```

Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
    565   570   575

Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
    580   585   590

Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
    595   600   605

Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
    610   615   620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr
625   630   635   640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
    645   650   655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
    660   665   670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln
    675   680   685

Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala Pro
    690   695   700

Glu Asp Lys Thr Gln Glu Ala Glu
705   710

<210> 155

<211> 3456

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (281)..(3016)

<400> 155

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agcattcaag gagctcccca ggagaaagag caagttctga ggagccctct gagcccggaa   60

cgtgtccacc cggtcatgcc cgccgcgcac cagccccgca gtggacttgg aggaggagga  120

ggaggagagc tctgtggatg gcaaagggga ccggaagagc acaggcctga aactctccaa  180

gaagaaagca aggaggagac acacggatga cccaagcaag gaatgcttca ctctgaaatt  240

tgacctgaat gtggacattg agacagagat cgtcccagcc atg aag aag aag tca   295
                                               Met Lys Lys Lys Ser
                                                1               5

ctg ggg gag gtg ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg   343
Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu
            10                  15                  20
```

```
ggc aaa gtg gac atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc     391
Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu
            25                  30                  35


acc ttc gag gcc tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc     439
Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala
            40                  45                  50


cca gcc aag cct gga gat gag ggc aag gtg gag cag ggc atg aag gac     487
Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp
            55                  60                  65


tcc aag tcc ctg agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc     535
Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro
    70                  75                  80                  85


ccc gcc ctg gag cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac     583
Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp
                90                  95                  100


atc ttg gcc cct ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg     631
Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly
                105                 110                 115


gag gcg agc atc ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct     679
Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser
                120                 125                 130


ctg ccc agc ggc agc agt ggc agc acc aac act ggc gac agc tgg aag     727
```

Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys
    135   140   145

aac cgg gcg gcc agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc   775
Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser
150   155   160   165

acc agc gcc ttt ggc cgg gag gta gac aag atg gag cag ctg gag ggc   823
Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly
                170   175   180

aag ctg cac acc tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg   871
Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly
                185   190   195

ctg cgc ttc gac cat gac tcc tgg gag gag gag tac gat gaa gac gag   919
Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu
        200   205   210

gat gag gac aat gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc   967
Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu
        215   220   225

att gat ggg cat gag aag ctg acc cgg cgg cag tgc cac cag cag gag   1015
Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu
230   235   240   245

gcg gtg tgg gag ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg   1063
Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu

```
                 250                    255                    260


cgg gtg atc atc aac ctg ttc ttg tgc tgc ctc ctg aac ctg caa gag   1111
Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu
             265                    270                    275


tca ggg ctg ctg tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc   1159
Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile
             280                    285                    290


ccg gag atc gcg cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg   1207
Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala
             295                    300                    305


ccg gtg ctg gag aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg   1255
Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly
310                    315                    320                    325


gac ttc ctc aaa ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac   1303
Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr
             330                    335                    340


atc cgc tac tgc atg gag gag gag ggc tgc atg gag tac atg cgc ggc   1351
Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly
             345                    350                    355


ctg ctg cgc gac aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag   1399
Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu
             360                    365                    370
```

```
aag cac cca cag tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa    1447
Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys
    375             380             385
```

```
ccc cac cag cgg ctc acc aag tac ccg ctg ctg ctc aag tcg gtg ctg    1495
Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu
390             395             400             405
```

```
agg aag acc gag gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc    1543
Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile
            410             415             420
```

```
ggc tcc gtg gag cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag    1591
Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln
            425             430             435
```

```
cgg cag gag cgg cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc    1639
Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala
    440             445             450
```

```
tac gag gtg gtg gaa agc agc agc gac gaa gtg gac aag ctc ctg aag    1687
Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys
    455             460             465
```

```
gaa ttt ctg cac ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg    1735
Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro
470             475             480             485
```

gag gag acg cgg cag ctg ctg ctg gag ggg agc ctg agg atg aag gag   1783
Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu
           490   495   500

ggg aag gac agc aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg   1831
Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu
           505   510   515

ctg ttg gtg acc aaa gca gtg aag aag gca gag agg acc agg gtc atc   1879
Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile
           520   525   530

agg cca ccc ctg ctc gtg gac aag att gtg tgc cgg gag cta cgg gac   1927
Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp
           535   540   545

cct ggg tcc ttc ctc ctt atc tac ctg aat gag ttt cac agt gct gta   1975
Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val
550   555   560   565

ggg gcc tac acg ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg   2023
Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp
           570   575   580

gtg gac acc att tac aat gcc cag aac cag ctg caa cag ctg cgt gca   2071
Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala
           585   590   595

cag gag ccc cca ggc agt cag cag ccc ctg cag agc ctg gaa gag gag   2119

Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu
　　　　 600　　　　　　　　　 605　　　　　　　　　 610

gag gat gag cag gag gag gaa gag gag gag gag gag gag gag gag gaa　2167
Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
　　　 615　　　　　　　　 620　　　　　　　　 625

ggc gag gac agt ggc act tca gct gcc agc tcc cct acc atc atg cgg　2215
Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg
630　　　　　　　 635　　　　　　　 640　　　　　　　 645

aaa agc agc ggc agc ccc gac tct cag cac tgt gcc tca gat ggc tcc　2263
Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser
　　　　　　　　 650　　　　　　　 655　　　　　　　 660

acg gag acc ctg gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc　2311
Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser
　　　　　　 665　　　　　　　 670　　　　　　　 675

tcc ccc gag ttc gac agc ggt cct ttc agc tcc cag tct gat gag acc　2359
Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr
　　　　　　 680　　　　　　　 685　　　　　　　 690

tct ctc agc acc act gcc tca tct gcc acg ccc acc agt gag ctg ctg　2407
Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu
　　　　　　 695　　　　　　　 700　　　　　　　 705

ccc ctg ggt ccg gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac　2455
Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr

710   715   720   725

```
ggc acc ctc tcc cca acc tcc tta caa gac ttt gtg gcc cca ggc cca    2503
Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro
                730                735                740
```

```
atg gca gag cta gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc    2551
Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser
                745                750                755
```

```
cct cca ccc tcg ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg    2599
Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu
                760                765                770
```

```
agc tgc ccg ccc cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc    2647
Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu
                775                780                785
```

```
cag ctg ctg gca ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc    2695
Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser
790                795                800                805
```

```
cgc agc ctg tca gag ctc tgc ctg gct gtt cca gcc cca ggt att agg    2743
Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg
                810                815                820
```

```
act cag ggc tcc cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg    2791
Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly
                825                830                835
```

```
gcc cct agc cct ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg    2839
Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly
    840               845               850


gaa cct gca ggc tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg    2887
Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly
    855               860               865


gcc tct ccc agg gtc cag cct gag ccc cca cca ggg gtc tct gcc cag    2935
Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln
870               875               880               885


cac agg aag ctg acc ctg gcc cag ctc tac cga atc agg acc acc ctg    2983
His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu
              890               895               900


ctg ctt aac tcc acg ctc act gcc tcg gag gtc tgagcagagg gaggccccca 3036
Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
              905               910


agagtgccat tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc 3096


ttcagctact gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc 3156


gggcccgatt tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca 3216


ccccacctgc ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag 3276
```

tcttcagggc tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg 3336

gattcactcc tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg 3396

ggttctgtga agttacgtat ttattgagct tttggttctt ttataaagac ttgtctagac 3456

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<211> 912

<212> PRT

<213> Homo sapiens

<400> 156

Met Lys Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg
1   5   10   15

Lys Gly Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn
                20   25   30

Thr Pro Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr
            35   40   45

Leu Arg Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu
        50   55   60

Gln Gly Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro
65   70   75   80

Ala Gly Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg

```
                  85                    90                    95

Arg Glu Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met
              100                   105                   110


Ser Glu Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr
              115                   120                   125


Pro Ser Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr
              130                   135                   140


Gly Asp Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe
145                   150                   155                   160


Ser Ser Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met
                  165                   170                   175


Glu Gln Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro
                  180                   185                   190


Arg Leu Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu
                  195                   200                   205


Tyr Asp Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp
210                   215                   220


Ser Trp Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln
225                   230                   235                   240
```

Cys His Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser
              245   250   255

Tyr Ile Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu
              260   265   270

Leu Asn Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg
              275   280   285

Leu Phe Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp
              290   295   300

Ala Ser Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala
305   310   315   320

Leu Leu Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser
              325   330   335

Leu Phe Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met
              340   345   350

Glu Tyr Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr
              355   360   365

Ile Thr Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser
              370   375   380

Asp Met Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu
385   390   395   400

Leu Lys Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala
        405   410   415

Val Val Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn
        420   425   430

Ala Cys Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val
        435   440   445

Ser Arg Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val
    450   455   460

Asp Lys Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile
465   470   475   480

Pro Gly Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser
                485   490   495

Leu Arg Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe
        500   505   510

Leu Phe Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu
        515   520   525

Arg Thr Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys
    530   535   540

Arg Glu Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu

545   550   555   560

Phe His Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala
              565   570   575

Leu Cys Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu
              580   585   590

Gln Gln Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln
              595   600   605

Ser Leu Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu
              610   615   620

Glu Glu Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser
625   630   635   640

Pro Thr Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys
              645   650   655

Ala Ser Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro
              660   665   670

Gly Asp Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser
              675   680   685

Gln Ser Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro
              690   695   700

Thr Ser Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser
705   710   715   720

Met Asp Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe
                    725   730   735

Val Ala Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser
                    740   745   750

Pro Arg Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr
                    755   760   765

Pro Val Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser
                    770   775   780

Glu Ala Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr
785   790   795   800

Pro Ser Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro
                    805   810   815

Ala Pro Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser
                    820   825   830

Trp Asp Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val
                    835   840   845

Gly Cys Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly
850   855   860

Asp Leu Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro
865   870   875   880

Gly Val Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg
                   885   890   895

Ile Arg Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
              900   905   910

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<220>

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<400> 157

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ggatgtatgt caccacgccg actgccagca gctgcaccgc cggggccccc tcaacctctg 120

cgaggcctgt gacagcaagt tccacagcac c atg cat tat gat ggg cat gtc   172
                                  Met His Tyr Asp Gly His Val
                                  1   5

```
cgc ttc gac ctt ccc cca caa ggc tct gtg ctg gcc cgg aac gtg tcc    220
Arg Phe Asp Leu Pro Pro Gln Gly Ser Val Leu Ala Arg Asn Val Ser
         10                  15                  20


acc cgg tca tgc ccg ccg cgc acc agc ccc gca gtg gac ttg gag gag    268
Thr Arg Ser Cys Pro Pro Arg Thr Ser Pro Ala Val Asp Leu Glu Glu
         25                  30                  35


gag gag gag gag agc tct gtg gat ggc aaa ggg gac cgg aag agc aca    316
Glu Glu Glu Glu Ser Ser Val Asp Gly Lys Gly Asp Arg Lys Ser Thr
 40                  45                  50                  55


ggc ctg aaa ctc tcc aag aag aaa gca agg agg aga cac acg gat gac    364
Gly Leu Lys Leu Ser Lys Lys Lys Ala Arg Arg Arg His Thr Asp Asp
                 60                  65                  70


cca agc aag gaa tgc ttc act ctg aaa ttt gac ctg aat gtg gac att    412
Pro Ser Lys Glu Cys Phe Thr Leu Lys Phe Asp Leu Asn Val Asp Ile
             75                  80                  85


gag aca gag atc gtc cca gcc atg aag aag aag tca ctg ggg gag gtg    460
Glu Thr Glu Ile Val Pro Ala Met Lys Lys Lys Ser Leu Gly Glu Val
         90                  95                 100


ctg ctg cct gta ttt gaa agg aag ggc att gcg ctg ggc aaa gtg gac    508
Leu Leu Pro Val Phe Glu Arg Lys Gly Ile Ala Leu Gly Lys Val Asp
        105                 110                 115
```

```
atc tac ctg gac cag tcc aac aca ccc ctg tcc ctc acc ttc gag gcc    556
Ile Tyr Leu Asp Gln Ser Asn Thr Pro Leu Ser Leu Thr Phe Glu Ala
120             125             130             135


tac agg ttc ggg gga cac tac ctt cgt gtc aaa gcc cca gcc aag cct    604
Tyr Arg Phe Gly Gly His Tyr Leu Arg Val Lys Ala Pro Ala Lys Pro
            140             145             150


gga gat gag ggc aag gtg gag cag ggc atg aag gac tcc aag tcc ctg    652
Gly Asp Glu Gly Lys Val Glu Gln Gly Met Lys Asp Ser Lys Ser Leu
            155             160             165


agt ttg ccg att ctg cgg cca gct ggg acc ggg ccc ccc gcc ctg gag    700
Ser Leu Pro Ile Leu Arg Pro Ala Gly Thr Gly Pro Pro Ala Leu Glu
            170             175             180


cgt gtg gac gcc cag agc cgc cgg gag agc ctg gac atc ttg gcc cct    748
Arg Val Asp Ala Gln Ser Arg Arg Glu Ser Leu Asp Ile Leu Ala Pro
            185             190             195


ggc cgc cgc cgc aag aac atg tcg gag ttc ctg ggg gag gcg agc atc    796
Gly Arg Arg Arg Lys Asn Met Ser Glu Phe Leu Gly Glu Ala Ser Ile
200             205             210             215


ccc ggg cag gag ccc ccc acg ccc tcc agc tgc tct ctg ccc agc ggc    844
Pro Gly Gln Glu Pro Pro Thr Pro Ser Ser Cys Ser Leu Pro Ser Gly
            220             225             230


agc agt ggc agc acc aac act ggc gac agc tgg aag aac cgg gcg gcc    892
```

Ser Ser Gly Ser Thr Asn Thr Gly Asp Ser Trp Lys Asn Arg Ala Ala

        235   240   245

agt cgc ttc agc ggc ttt ttc agc tcc ggc ccc agc acc agc gcc ttt   940

Ser Arg Phe Ser Gly Phe Phe Ser Ser Gly Pro Ser Thr Ser Ala Phe

        250   255   260

ggc cgg gag gta gac aag atg gag cag ctg gag ggc aag ctg cac acc   988

Gly Arg Glu Val Asp Lys Met Glu Gln Leu Glu Gly Lys Leu His Thr

        265   270   275

tac agc ctc ttc ggg ctg ccc agg ctg ccc cgg ggg ctg cgc ttc gac   1036

Tyr Ser Leu Phe Gly Leu Pro Arg Leu Pro Arg Gly Leu Arg Phe Asp

280   285   290   295

cat gac tcc tgg gag gag gag tac gat gaa gac gag gat gag gac aat   1084

His Asp Ser Trp Glu Glu Glu Tyr Asp Glu Asp Glu Asp Glu Asp Asn

           300   305   310

gcc tgc ctg agg ctg gag gac agc tgg cgg gag ctc att gat ggg cat   1132

Ala Cys Leu Arg Leu Glu Asp Ser Trp Arg Glu Leu Ile Asp Gly His

        315   320   325

gag aag ctg acc cgg cgg cag tgc cac cag cag gag gcg gtg tgg gag   1180

Glu Lys Leu Thr Arg Arg Gln Cys His Gln Gln Glu Ala Val Trp Glu

        330   335   340

ctg ctg cac acg gag gcc tcc tac atc agg aaa ctg cgg gtg atc atc   1228

Leu Leu His Thr Glu Ala Ser Tyr Ile Arg Lys Leu Arg Val Ile Ile

345   350   355

```
aac ctg ttc ctg tgc tgc ctc ctg aac ctg caa gag tca ggg ctg ctg    1276
Asn Leu Phe Leu Cys Cys Leu Leu Asn Leu Gln Glu Ser Gly Leu Leu
360             365             370             375
```

```
tgt gag gtg gag gcg gag cgc ctg ttc agc aac atc ccg gag atc gcg    1324
Cys Glu Val Glu Ala Glu Arg Leu Phe Ser Asn Ile Pro Glu Ile Ala
                380             385             390
```

```
cag ctg cac cgc agg ctg tgg gct agc gtg atg gcg ccg gtg ctg gag    1372
Gln Leu His Arg Arg Leu Trp Ala Ser Val Met Ala Pro Val Leu Glu
                395             400             405
```

```
aag gcg cgg cgc acg cga gcg ctg cta cag ccc ggg gac ttc ctc aaa    1420
Lys Ala Arg Arg Thr Arg Ala Leu Leu Gln Pro Gly Asp Phe Leu Lys
                410             415             420
```

```
ggc ttc aag atg ttc ggc tcg ctc ttc aag ccc tac atc cgc tac tgc    1468
Gly Phe Lys Met Phe Gly Ser Leu Phe Lys Pro Tyr Ile Arg Tyr Cys
                425             430             435
```

```
atg gag gag gag ggc tgc atg gag tac atg cgc ggc ctg ctg cgc gac    1516
Met Glu Glu Glu Gly Cys Met Glu Tyr Met Arg Gly Leu Leu Arg Asp
440             445             450             455
```

```
aac gac ctc ttc cgg gcc tac atc acg tgg gcg gag aag cac cca cag    1564
Asn Asp Leu Phe Arg Ala Tyr Ile Thr Trp Ala Glu Lys His Pro Gln
                460             465             470
```

tgc cag agg ctg aag ctg agc gac atg ctg gcc aaa ccc cac cag cgg　　1612
Cys Gln Arg Leu Lys Leu Ser Asp Met Leu Ala Lys Pro His Gln Arg
　　　　　　　　475　　　　　　　　　480　　　　　　　　　485

ctc acc aag tac ccg ctg ctc ctc aag tcg gtg ctg agg aag acc gag　　1660
Leu Thr Lys Tyr Pro Leu Leu Leu Lys Ser Val Leu Arg Lys Thr Glu
　　　　　　　　490　　　　　　　　　495　　　　　　　　　500

gag ccg cgc gcc aag gag gcc gtc gtc gcc atg atc ggc tcc gtg gag　　1708
Glu Pro Arg Ala Lys Glu Ala Val Val Ala Met Ile Gly Ser Val Glu
　　　　　505　　　　　　　　　510　　　　　　　　　515

cgc ttc atc cac cac gtg aac gcg tgc atg cgg cag cgg cag gag cgg　　1756
Arg Phe Ile His His Val Asn Ala Cys Met Arg Gln Arg Gln Glu Arg
　520　　　　　　　　　525　　　　　　　　　530　　　　　　　　　535

cag cgg ctg gcg gcc gtg gtg agc cgc atc gac gcc tac gag gtg gtg　　1804
Gln Arg Leu Ala Ala Val Val Ser Arg Ile Asp Ala Tyr Glu Val Val
　　　　　　　　540　　　　　　　　　545　　　　　　　　　550

gaa agc agc agc gac gaa gtg gac aag ctc ctg aag gaa ttt ctg cac　　1852
Glu Ser Ser Ser Asp Glu Val Asp Lys Leu Leu Lys Glu Phe Leu His
　　　　　　　　555　　　　　　　　　560　　　　　　　　　565

ctg gac ttg aca gcg ccc atc cct ggc gcc tcc ccg gag gag acg cgg　　1900
Leu Asp Leu Thr Ala Pro Ile Pro Gly Ala Ser Pro Glu Glu Thr Arg
　　　　　　　　570　　　　　　　　　575　　　　　　　　　580

cag ctg ctg ctg gag ggg agc ctg agg atg aag gag ggg aag gac agc   1948
Gln Leu Leu Leu Glu Gly Ser Leu Arg Met Lys Glu Gly Lys Asp Ser
    585   590   595

aag atg gat gtg tac tgc ttc ctc ttc acg gat ctg ctg ttg gtg acc   1996
Lys Met Asp Val Tyr Cys Phe Leu Phe Thr Asp Leu Leu Leu Val Thr
600   605   610   615

aaa gca gtg aag aag gca gag agg acc agg gtc atc agg cca ccc ctg   2044
Lys Ala Val Lys Lys Ala Glu Arg Thr Arg Val Ile Arg Pro Pro Leu
                    620   625   630

ctc gtg gac aag att gtg tgc cgg gag cta cgg gac cct ggg tcc ttc   2092
Leu Val Asp Lys Ile Val Cys Arg Glu Leu Arg Asp Pro Gly Ser Phe
                    635   640   645

ctc ctt atc tac ctg aat gag ttt cac agt gct gta ggg gcc tac acg   2140
Leu Leu Ile Tyr Leu Asn Glu Phe His Ser Ala Val Gly Ala Tyr Thr
                650   655   660

ttc cag gcc agt ggc cag gcc ttg tgc cgt ggc tgg gtg gac acc att   2188
Phe Gln Ala Ser Gly Gln Ala Leu Cys Arg Gly Trp Val Asp Thr Ile
    665   670   675

tac aat gcc cag aac cag ctg caa cag ctg cgt gca cag gag ccc cca   2236
Tyr Asn Ala Gln Asn Gln Leu Gln Gln Leu Arg Ala Gln Glu Pro Pro
680   685   690   695

ggc agt cag cag ccc ctg cag agc ctg gaa gag gag gag gat gag cag   2284

Gly Ser Gln Gln Pro Leu Gln Ser Leu Glu Glu Glu Glu Asp Glu Gln
         700   705   710

gag gag gaa gag gag gag gag gag gag gag gag gaa ggc gag gac agt   2332
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Glu Asp Ser
         715   720   725

ggc act tca gct gcc agc tcc cct acc atc atg cgg aaa agc agc ggc   2380
Gly Thr Ser Ala Ala Ser Ser Pro Thr Ile Met Arg Lys Ser Ser Gly
         730   735   740

agc ccc gac tct cag cac tgt gcc tca gat ggc tcc acg gag acc ctg   2428
Ser Pro Asp Ser Gln His Cys Ala Ser Asp Gly Ser Thr Glu Thr Leu
         745   750   755

gcc atg gtt gtg gta gag cct ggg gac acg ctg tcc tcc ccc gag ttc   2476
Ala Met Val Val Val Glu Pro Gly Asp Thr Leu Ser Ser Pro Glu Phe
760   765   770   775

gac agc ggt cct ttc agc tcc cag tct gat gag acc tct ctc agc acc   2524
Asp Ser Gly Pro Phe Ser Ser Gln Ser Asp Glu Thr Ser Leu Ser Thr
            780   785   790

act gcc tca tct gcc acg ccc acc agt gag ctg ctg ccc ctg ggt ccg   2572
Thr Ala Ser Ser Ala Thr Pro Thr Ser Glu Leu Leu Pro Leu Gly Pro
            795   800   805

gtg gac ggc cgc tcc tgc tcc atg gac tct gcc tac ggc acc ctc tcc   2620
Val Asp Gly Arg Ser Cys Ser Met Asp Ser Ala Tyr Gly Thr Leu Ser

810   815   820

```
cca acc tcc tta caa gac ttt gtg gcc cca ggc cca atg gca gag cta    2668
Pro Thr Ser Leu Gln Asp Phe Val Ala Pro Gly Pro Met Ala Glu Leu
    825             830             835
```

```
gtg cct cgg gcc cca gag tcc cca cga gtt cct tcc cct cca ccc tcg    2716
Val Pro Arg Ala Pro Glu Ser Pro Arg Val Pro Ser Pro Pro Pro Ser
840             845             850             855
```

```
ccc cgt ctc cgc cgc cgc acc cct gtc cag ctg ttg agc tgc ccg ccc    2764
Pro Arg Leu Arg Arg Arg Thr Pro Val Gln Leu Leu Ser Cys Pro Pro
            860             865             870
```

```
cac ctg ctc aag tct aag tcc gag gcc agc ctc ctc cag ctg ctg gca    2812
His Leu Leu Lys Ser Lys Ser Glu Ala Ser Leu Leu Gln Leu Leu Ala
            875             880             885
```

```
ggg gct ggc acc cat ggg aca ccc tct gcc ccc agc cgc agc ctg tca    2860
Gly Ala Gly Thr His Gly Thr Pro Ser Ala Pro Ser Arg Ser Leu Ser
        890             895             900
```

```
gag ctc tgc ctg gct gtt cca gcc cca ggt att agg act cag ggc tcc    2908
Glu Leu Cys Leu Ala Val Pro Ala Pro Gly Ile Arg Thr Gln Gly Ser
    905             910             915
```

```
cct cag gaa gct ggg ccc agc tgg gat tgc cga ggg gcc cct agc cct    2956
Pro Gln Glu Ala Gly Pro Ser Trp Asp Cys Arg Gly Ala Pro Ser Pro
920             925             930             935
```

ggc agc ggt cct ggg cta gtc ggc tgc ctg gcc ggg gaa cct gca ggc   3004
Gly Ser Gly Pro Gly Leu Val Gly Cys Leu Ala Gly Glu Pro Ala Gly
              940   945   950

tcc cac agg aag agg tgt gga gac ctg ccc tcg ggg gcc tct ccc agg   3052
Ser His Arg Lys Arg Cys Gly Asp Leu Pro Ser Gly Ala Ser Pro Arg
              955   960   965

gtc cag cct gag ccc cca cca ggg gtc tct gcc cag cac agg aag ctg   3100
Val Gln Pro Glu Pro Pro Pro Gly Val Ser Ala Gln His Arg Lys Leu
              970   975   980

acc ctg gcc cag ctc tac cga atc agg acc acc ctg ctg ctt aac tcc   3148
Thr Leu Ala Gln Leu Tyr Arg Ile Arg Thr Thr Leu Leu Leu Asn Ser
              985   990   995

acg ctc act gcc tcg gag gtc tgagcagagg gaggccccca agagtgccat   3199
Thr Leu Thr Ala Ser Glu Val
1000   1005

tgaccaagag acagcagaca gcctgcctcc tggggcgtgc cggcacctgc ttcagctact 3259

gcctcctgta tgcatgagcc ggatgctggg caggatccct gcctacgccc gggcccgatt 3319

tgcgctttgc cggactggat ggagtggagg aggcccaggc cacagtacca ccccacctgc 3379

ccaggcagcc cctcgtcacc tactccccga agttaccagc tcagctcgag tcttcagggc 3439

tgggctccta ggctgcccat cctacttcta ccctcactgg cctccagtgg gattcactcc 3499

tgccctgccc ccaccttccc agtcccacag gccacccctg gcttgggctg ggttctgtga 3559

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<210> 158

<211> 1006

<212> PRT

<213> Homo sapiens

<400> 158

Met	His	Tyr	Asp	Gly	His	Val	Arg	Phe	Asp	Leu	Pro	Pro	Gln	Gly	Ser
1				5					10				15		

Val	Leu	Ala	Arg	Asn	Val	Ser	Thr	Arg	Ser	Cys	Pro	Pro	Arg	Thr	Ser
			20				25				30				

Pro	Ala	Val	Asp	Leu	Glu	Glu	Glu	Glu	Glu	Ser	Ser	Val	Asp	Gly
		35				40				45				

Lys	Gly	Asp	Arg	Lys	Ser	Thr	Gly	Leu	Lys	Leu	Ser	Lys	Lys	Lys	Ala
	50				55				60						

Arg	Arg	Arg	His	Thr	Asp	Asp	Pro	Ser	Lys	Glu	Cys	Phe	Thr	Leu	Lys
65				70				75				80			

Phe	Asp	Leu	Asn	Val	Asp	Ile	Glu	Thr	Glu	Ile	Val	Pro	Ala	Met	Lys

                85   90   95

Lys Lys Ser Leu Gly Glu Val Leu Leu Pro Val Phe Glu Arg Lys Gly
            100   105   110

Ile Ala Leu Gly Lys Val Asp Ile Tyr Leu Asp Gln Ser Asn Thr Pro
            115   120   125

Leu Ser Leu Thr Phe Glu Ala Tyr Arg Phe Gly Gly His Tyr Leu Arg
            130   135   140

Val Lys Ala Pro Ala Lys Pro Gly Asp Glu Gly Lys Val Glu Gln Gly
145   150   155   160

Met Lys Asp Ser Lys Ser Leu Ser Leu Pro Ile Leu Arg Pro Ala Gly
                165   170   175

Thr Gly Pro Pro Ala Leu Glu Arg Val Asp Ala Gln Ser Arg Arg Glu
                180   185   190

Ser Leu Asp Ile Leu Ala Pro Gly Arg Arg Arg Lys Asn Met Ser Glu
                195   200   205

Phe Leu Gly Glu Ala Ser Ile Pro Gly Gln Glu Pro Pro Thr Pro Ser
            210   215   220

Ser Cys Ser Leu Pro Ser Gly Ser Ser Gly Ser Thr Asn Thr Gly Asp
225   230   235   240

Ser Trp Lys Asn Arg Ala Ala Ser Arg Phe Ser Gly Phe Phe Ser Ser
          245   250   255

Gly Pro Ser Thr Ser Ala Phe Gly Arg Glu Val Asp Lys Met Glu Gln
          260   265   270

Leu Glu Gly Lys Leu His Thr Tyr Ser Leu Phe Gly Leu Pro Arg Leu
          275   280   285

Pro Arg Gly Leu Arg Phe Asp His Asp Ser Trp Glu Glu Glu Tyr Asp
          290   295   300

Glu Asp Glu Asp Glu Asp Asn Ala Cys Leu Arg Leu Glu Asp Ser Trp
305   310   315   320

Arg Glu Leu Ile Asp Gly His Glu Lys Leu Thr Arg Arg Gln Cys His
              325   330   335

Gln Gln Glu Ala Val Trp Glu Leu Leu His Thr Glu Ala Ser Tyr Ile
              340   345   350

Arg Lys Leu Arg Val Ile Ile Asn Leu Phe Leu Cys Cys Leu Leu Asn
          355   360   365

Leu Gln Glu Ser Gly Leu Leu Cys Glu Val Glu Ala Glu Arg Leu Phe
          370   375   380

Ser Asn Ile Pro Glu Ile Ala Gln Leu His Arg Arg Leu Trp Ala Ser
385   390   395   400

Val Met Ala Pro Val Leu Glu Lys Ala Arg Arg Thr Arg Ala Leu Leu
               405   410   415

Gln Pro Gly Asp Phe Leu Lys Gly Phe Lys Met Phe Gly Ser Leu Phe
               420   425   430

Lys Pro Tyr Ile Arg Tyr Cys Met Glu Glu Glu Gly Cys Met Glu Tyr
               435   440   445

Met Arg Gly Leu Leu Arg Asp Asn Asp Leu Phe Arg Ala Tyr Ile Thr
               450   455   460

Trp Ala Glu Lys His Pro Gln Cys Gln Arg Leu Lys Leu Ser Asp Met
465   470   475   480

Leu Ala Lys Pro His Gln Arg Leu Thr Lys Tyr Pro Leu Leu Leu Lys
               485   490   495

Ser Val Leu Arg Lys Thr Glu Glu Pro Arg Ala Lys Glu Ala Val Val
               500   505   510

Ala Met Ile Gly Ser Val Glu Arg Phe Ile His His Val Asn Ala Cys
               515   520   525

Met Arg Gln Arg Gln Glu Arg Gln Arg Leu Ala Ala Val Val Ser Arg
               530   535   540

Ile Asp Ala Tyr Glu Val Val Glu Ser Ser Ser Asp Glu Val Asp Lys

```
      545                  550                  555                  560
```

Leu Leu Lys Glu Phe Leu His Leu Asp Leu Thr Ala Pro Ile Pro Gly

```
                        565                  570                  575
```

Ala Ser Pro Glu Glu Thr Arg Gln Leu Leu Leu Glu Gly Ser Leu Arg

```
                        580                  585                  590
```

Met Lys Glu Gly Lys Asp Ser Lys Met Asp Val Tyr Cys Phe Leu Phe

```
                        595                  600                  605
```

Thr Asp Leu Leu Leu Val Thr Lys Ala Val Lys Lys Ala Glu Arg Thr

```
      610                  615                  620
```

Arg Val Ile Arg Pro Pro Leu Leu Val Asp Lys Ile Val Cys Arg Glu

```
      625                  630                  635                  640
```

Leu Arg Asp Pro Gly Ser Phe Leu Leu Ile Tyr Leu Asn Glu Phe His

```
                        645                  650                  655
```

Ser Ala Val Gly Ala Tyr Thr Phe Gln Ala Ser Gly Gln Ala Leu Cys

```
                        660                  665                  670
```

Arg Gly Trp Val Asp Thr Ile Tyr Asn Ala Gln Asn Gln Leu Gln Gln

```
                        675                  680                  685
```

Leu Arg Ala Gln Glu Pro Pro Gly Ser Gln Gln Pro Leu Gln Ser Leu

```
                        690                  695                  700
```

Glu Glu Glu Glu Asp Glu Gln Glu Glu Glu Glu Glu Glu Glu Glu Glu
705 710 715 720

Glu Glu Glu Gly Glu Asp Ser Gly Thr Ser Ala Ala Ser Ser Pro Thr
725 730 735

Ile Met Arg Lys Ser Ser Gly Ser Pro Asp Ser Gln His Cys Ala Ser
740 745 750

Asp Gly Ser Thr Glu Thr Leu Ala Met Val Val Val Glu Pro Gly Asp
755 760 765

Thr Leu Ser Ser Pro Glu Phe Asp Ser Gly Pro Phe Ser Ser Gln Ser
770 775 780

Asp Glu Thr Ser Leu Ser Thr Thr Ala Ser Ser Ala Thr Pro Thr Ser
785 790 795 800

Glu Leu Leu Pro Leu Gly Pro Val Asp Gly Arg Ser Cys Ser Met Asp
805 810 815

Ser Ala Tyr Gly Thr Leu Ser Pro Thr Ser Leu Gln Asp Phe Val Ala
820 825 830

Pro Gly Pro Met Ala Glu Leu Val Pro Arg Ala Pro Glu Ser Pro Arg
835 840 845

Val Pro Ser Pro Pro Pro Ser Pro Arg Leu Arg Arg Arg Thr Pro Val
850 855 860

Gln Leu Leu Ser Cys Pro Pro His Leu Leu Lys Ser Lys Ser Glu Ala
865   870   875   880

Ser Leu Leu Gln Leu Leu Ala Gly Ala Gly Thr His Gly Thr Pro Ser
          885   890   895

Ala Pro Ser Arg Ser Leu Ser Glu Leu Cys Leu Ala Val Pro Ala Pro
          900   905   910

Gly Ile Arg Thr Gln Gly Ser Pro Gln Glu Ala Gly Pro Ser Trp Asp
          915   920   925

Cys Arg Gly Ala Pro Ser Pro Gly Ser Gly Pro Gly Leu Val Gly Cys
          930   935   940

Leu Ala Gly Glu Pro Ala Gly Ser His Arg Lys Arg Cys Gly Asp Leu
945   950   955   960

Pro Ser Gly Ala Ser Pro Arg Val Gln Pro Glu Pro Pro Pro Gly Val
          965   970   975

Ser Ala Gln His Arg Lys Leu Thr Leu Ala Gln Leu Tyr Arg Ile Arg
          980   985   990

Thr Thr Leu Leu Leu Asn Ser Thr Leu Thr Ala Ser Glu Val
          995   1000   1005

<210> 159

<211> 3168

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (93)..(3089)

<400> 159

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cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag   113

                                          Met Gly Trp Lys Pro Ser Glu

                                     1   5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg   161

Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg

        10   15   20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga   209

Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg

        25   30   35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg   257

Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

40   45   50   55

```
ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac     305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
                60              65              70


ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc     353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
           75              80              85


agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc     401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
                90              95              100


acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg     449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
           105             110             115


ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt     497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120             125             130             135


gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt     545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
                140             145             150


gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag     593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
                155             160             165


cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc     641
```

His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
    170   175   180

cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg   689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
    185   190   195

ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg   737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200   205   210   215

ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc   785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
          220   225   230

cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg   833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
          235   240   245

gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg   881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
       250   255   260

gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac   929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
     265   270   275

cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt   977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser

```
            280                 285                 290                 295

gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg   1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                    300                 305                 310

gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac   1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
                    315                 320                 325

ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc   1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
                330                 335                 340

acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg   1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
            345                 350                 355

acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc   1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
        360                 365                 370                 375

gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag   1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
                    380                 385                 390

gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc   1313
Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
                    395                 400                 405
```

```
gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca    1361
Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
         410                 415                 420


gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac    1409
Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
         425                 430                 435


cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag    1457
Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
440                 445                 450                 455


aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag    1505
Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
                 460                 465                 470


agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt    1553
Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
                 475                 480                 485


aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg    1601
Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
                 490                 495                 500


gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg    1649
Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
         505                 510                 515
```

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg　　1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
520　　　　　525　　　　　530　　　　　535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg　　1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
　　　　　540　　　　　545　　　　　550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg　　1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
　　　　　555　　　　　560　　　　　565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg　　1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
　　　　　570　　　　　575　　　　　580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt　　1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
　　　　　585　　　　　590　　　　　595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc　　1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600　　　　　605　　　　　610　　　　　615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag　　1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
　　　　　620　　　　　625　　　　　630

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg　　2033

672　　　　　　　　　出証特２００２－３０３２９３５

```
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
        635             640             645
```

```
ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att   2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
        650             655             660
```

```
ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc   2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
        665             670             675
```

```
acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag   2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680             685             690             695
```

```
atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag   2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
        700             705             710
```

```
ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg   2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
        715             720             725
```

```
gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag   2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
        730             735             740
```

```
gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg   2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
```

```
        745              750              755

ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg  2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760              765              770              775


ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg  2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
              780              785              790


gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg  2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
              795              800              805


agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag  2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
              810              815              820


ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag  2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
              825              830              835


cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg  2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840              845              850              855


acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc  2705
Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
              860              865              870
```

```
gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg    2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
        875              880              885


ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg    2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
        890              895              900


atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc    2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
    905              910              915


cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg    2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
920              925              930              935


cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa    2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
            940              945              950


cgc atc acc tgc ccc atc tgc atc gac agg cac atc cgc ctc gtg ttc    2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Arg His Ile Arg Leu Val Phe
            955              960              965


cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc    3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala
            970              975              980
```

```
tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg    3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
    985                 990                 995


tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgtttttata    3149


aaaagaaaga ttctcggat                                                   3168
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<210> 160

<211> 999

<212> PRT

<213> Homo sapiens

<400> 160

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Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
1               5                   10                  15


Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
            20                  25                  30


Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
            35                  40                  45


Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
        50                  55                  60


Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65                  70                  75                  80
```

出証特2002-3032935

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
　　　　　　　　85　　　　　　　　90　　　　　　　　95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
　　　　　　　100　　　　　　　105　　　　　　　　110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
　　　　　　　115　　　　　　　120　　　　　　　　125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
　　　　　　130　　　　　　　135　　　　　　　140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145　　　　　　　150　　　　　　　155　　　　　　　160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
　　　　　　　165　　　　　　　170　　　　　　　175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
　　　　　　　180　　　　　　　185　　　　　　　190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
　　　　　　　195　　　　　　　200　　　　　　　205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
　　　　　　210　　　　　　　215　　　　　　　220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg

225   230   235   240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
         245   250   255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
         260   265   270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
         275   280   285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
         290   295   300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305   310   315   320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
         325   330   335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
         340   345   350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
         355   360   365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu
         370   375   380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385   390   395   400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
              405   410   415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
              420   425   430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
              435   440   445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
              450   455   460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465   470   475   480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
              485   490   495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
              500   505   510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
              515   520   525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
              530   535   540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545   550   555   560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
                565   570   575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
                580   585   590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
                595   600   605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
                610   615   620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625   630   635   640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
                645   650   655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
                660   665   670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
                675   680   685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp

```
                690                    695                    700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
705                710                715                    720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
                725                    730                735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
                740                    745                750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
                755                    760                765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
     770                    775                780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
785                790                    795                800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
                805                    810                815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
                820                    825                830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro
     835                    840                845
```

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
   850   855   860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
865   870   875   880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
           885   890   895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
       900   905   910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
      915   920   925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
   930   935   940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945   950   955   960

Arg His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
       965   970   975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
       980   985   990

Asp Arg Ile Gln Ile Phe Val
   995

<210> 161

<211> 3168

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (93)..(3089)

<400> 161

agtgcccggt ggcccaggag ggcctgggag cccgaagccg tccccgagtc gctcctaggt 60

cactggcgcg atgcgggccg tcctctcggc tg atg ggt tgg aag ccc agc gag   113
                                     Met Gly Trp Lys Pro Ser Glu
                                     1   5

gct aga ggc cag tcc caa agt ctc cag gca tca ggg ctg cag ccc agg   161
Ala Arg Gly Gln Ser Gln Ser Leu Gln Ala Ser Gly Leu Gln Pro Arg
        10   15   20

agc ctc aag gcg gcc cgg cgg gcg act gga cgg ccg gac agg tcc cga   209
Ser Leu Lys Ala Ala Arg Arg Ala Thr Gly Arg Pro Asp Arg Ser Arg
        25   30   35

gca gcc ccg ccc aac atg gac cca gac ccc cag gcg ggc gtg cag gtg   257
Ala Ala Pro Pro Asn Met Asp Pro Asp Pro Gln Ala Gly Val Gln Val

```
            40                    45                    50                    55


ggc atg cgg gtg gtg cgc ggc gtg gac tgg aag tgg ggc cag cag gac    305
Gly Met Arg Val Val Arg Gly Val Asp Trp Lys Trp Gly Gln Gln Asp
                       60                    65                    70


ggc ggc gag ggc ggc gtg ggc acg gtg gtg gag ctt ggc cgc cac ggc    353
Gly Gly Glu Gly Gly Val Gly Thr Val Val Glu Leu Gly Arg His Gly
                  75                    80                    85


agc ccc tcg aca ccc gac cgc aca gtg gtc gtg cag tgg gac cag ggc    401
Ser Pro Ser Thr Pro Asp Arg Thr Val Val Val Gln Trp Asp Gln Gly
                  90                    95                   100


acg cgc acc aac tac cgc gcc ggc tac cag ggc gcg cac gac ctg ctg    449
Thr Arg Thr Asn Tyr Arg Ala Gly Tyr Gln Gly Ala His Asp Leu Leu
             105                   110                   115


ctg tac gac aac gcc cag atc ggc gtc cgg cac ccc aac atc atc tgt    497
Leu Tyr Asp Asn Ala Gln Ile Gly Val Arg His Pro Asn Ile Ile Cys
120                   125                   130                   135


gac tgc tgc aag aag cac ggg ctg cgg ggg atg cgc tgg aag tgc cgt    545
Asp Cys Cys Lys Lys His Gly Leu Arg Gly Met Arg Trp Lys Cys Arg
                       140                   145                   150


gtg tgc ctg gac tac gac ctc tgc acg cag tgc tac atg cac aac aag    593
Val Cys Leu Asp Tyr Asp Leu Cys Thr Gln Cys Tyr Met His Asn Lys
                  155                   160                   165
```

```
cat gag ctc gcc cac gcc ttc gac cgc tac gag acc gct cac tcg cgc   641
His Glu Leu Ala His Ala Phe Asp Arg Tyr Glu Thr Ala His Ser Arg
        170             175             180


cct gtc aca ctg agt ccc cgc cag ggc ctc ccg agg atc cca cta agg   689
Pro Val Thr Leu Ser Pro Arg Gln Gly Leu Pro Arg Ile Pro Leu Arg
        185             190             195


ggc atc ttc cag gga gcg aag gtg gtg cga ggc ccc ttc tgg gag tgg   737
Gly Ile Phe Gln Gly Ala Lys Val Val Arg Gly Pro Phe Trp Glu Trp
200             205             210             215


ggc tca cag gat gga ggg gaa ggg aaa ccg ggc cgt gtg gtg gac atc   785
Gly Ser Gln Asp Gly Gly Glu Gly Lys Pro Gly Arg Val Val Asp Ile
                220             225             230


cgt ggc tgg gat gtg gag aca ggc cgg agt gtg gcc agc gtg acg tgg   833
Arg Gly Trp Asp Val Glu Thr Gly Arg Ser Val Ala Ser Val Thr Trp
        235             240             245


gct gat ggt acc acc aat gtg tac cgt gtg ggc cac aag ggc aag gtg   881
Ala Asp Gly Thr Thr Asn Val Tyr Arg Val Gly His Lys Gly Lys Val
        250             255             260


gac ctc aag tgt gtg ggc gag gca gcg ggc ggc ttc tac tac aag gac   929
Asp Leu Lys Cys Val Gly Glu Ala Ala Gly Gly Phe Tyr Tyr Lys Asp
        265             270             275
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cac ctc cca agg ctc ggc aag ccg gcg gag ctg cag cgc agg gtg agt      977
His Leu Pro Arg Leu Gly Lys Pro Ala Glu Leu Gln Arg Arg Val Ser
280             285             290             295


gct gac agc cag ccc ttc cag cac ggg gac aag gtc aag tgt ctg ctg     1025
Ala Asp Ser Gln Pro Phe Gln His Gly Asp Lys Val Lys Cys Leu Leu
                300             305             310


gac act gat gtc ctg cgg gag atg cag gaa ggc cac ggc ggc tgg aac     1073
Asp Thr Asp Val Leu Arg Glu Met Gln Glu Gly His Gly Gly Trp Asn
                315             320             325


ccc agg atg gcg gag ttt atc gga cag acg ggc acc gtg cat cgt atc     1121
Pro Arg Met Ala Glu Phe Ile Gly Gln Thr Gly Thr Val His Arg Ile
                330             335             340


acg gac cgc ggg gac gtg cgc gtg cag ttc aac cac gag acg cgc tgg     1169
Thr Asp Arg Gly Asp Val Arg Val Gln Phe Asn His Glu Thr Arg Trp
345             350             355


acc ttc cac ccc ggg gcg ctc acc aag cac cac tcc ttc tgg gtg ggc     1217
Thr Phe His Pro Gly Ala Leu Thr Lys His His Ser Phe Trp Val Gly
360             365             370             375


gac gtg gtc cgg gtc atc ggc gac ctt gac aca gtg aag cgg ctg cag     1265
Asp Val Val Arg Val Ile Gly Asp Leu Asp Thr Val Lys Arg Leu Gln
                380             385             390


gct ggg cat ggc gag tgg acg gac gac atg gcc cct gcc ctg ggc cgc     1313
```

```
        Ala Gly His Gly Glu Trp Thr Asp Asp Met Ala Pro Ala Leu Gly Arg
                    395               400               405


        gtc ggg aag gtg gtg aaa gtg ttt gga gac ggg aac ctg cgt gta gca    1361
        Val Gly Lys Val Val Lys Val Phe Gly Asp Gly Asn Leu Arg Val Ala
                    410               415               420


        gtc gct ggt cag cgg tgg acc ttc agc ccc tcc tgc ctg gtg gcc tac    1409
        Val Ala Gly Gln Arg Trp Thr Phe Ser Pro Ser Cys Leu Val Ala Tyr
                    425               430               435


        cgg ccc gag gag gat gcc aac ctg gac gtg gcc gag cgc gcc cgg gag    1457
        Arg Pro Glu Glu Asp Ala Asn Leu Asp Val Ala Glu Arg Ala Arg Glu
        440               445               450               455


        aac aaa agc tca ctg agc gtg gcc ctg gac aag ctt cgg gcc cag aag    1505
        Asn Lys Ser Ser Leu Ser Val Ala Leu Asp Lys Leu Arg Ala Gln Lys
                          460               465               470


        agt gac cca gag cac ccg gga agg ctg gtg gtg gag gtg gcg ctg ggt    1553
        Ser Asp Pro Glu His Pro Gly Arg Leu Val Val Glu Val Ala Leu Gly
                    475               480               485


        aac gca gcc cgg gct ctg gac ctg ctg cgg agg cgc cca gag caa gtg    1601
        Asn Ala Ala Arg Ala Leu Asp Leu Leu Arg Arg Arg Pro Glu Gln Val
                    490               495               500


        gac acc aag aac caa ggc agg acc gct ctg caa gtg gct gcc tac ctg    1649
        Asp Thr Lys Asn Gln Gly Arg Thr Ala Leu Gln Val Ala Ala Tyr Leu
```

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                 505                      510                      515

ggc cag gtg gag ttg ata cgg ctg ctg cta caa gcc agg gcg ggc gtg    1697
Gly Gln Val Glu Leu Ile Arg Leu Leu Leu Gln Ala Arg Ala Gly Val
520                      525                      530                      535

gac ctg ccg gac gac gag ggc aac acg gca ctg cac tac gcg gcc ctg    1745
Asp Leu Pro Asp Asp Glu Gly Asn Thr Ala Leu His Tyr Ala Ala Leu
                         540                      545                      550

ggg aac cag ccc gag gcc acc agg gtg ctc ctg agt gct ggg tgc cgg    1793
Gly Asn Gln Pro Glu Ala Thr Arg Val Leu Leu Ser Ala Gly Cys Arg
                    555                      560                      565

gcg gac gcc atc aac agc acc cag agc aca gca ctg cac gtg gcc gtg    1841
Ala Asp Ala Ile Asn Ser Thr Gln Ser Thr Ala Leu His Val Ala Val
               570                      575                      580

cag agg ggc ttc ctg gag gtg gtg cgg gcc ctg tgt gag cgc ggc tgt    1889
Gln Arg Gly Phe Leu Glu Val Val Arg Ala Leu Cys Glu Arg Gly Cys
          585                      590                      595

gac gtc aac ctg ccc gac gcc cac tcg gac acg ccc ctg cac tcc gcc    1937
Asp Val Asn Leu Pro Asp Ala His Ser Asp Thr Pro Leu His Ser Ala
600                      605                      610                      615

atc tcg gcg ggc act gga gcc agc ggc att gtc gag gtc ctc acg gag    1985
Ile Ser Ala Gly Thr Gly Ala Ser Gly Ile Val Glu Val Leu Thr Glu
                    620                      625                      630
```

gtg cca aac atc gat gtt acc gcc acc aac agc cag ggt ttc acc ctg　2033
Val Pro Asn Ile Asp Val Thr Ala Thr Asn Ser Gln Gly Phe Thr Leu
　　　　　　　635　　　　　　　　　640　　　　　　　　　645

ctg cac cat gcc tcc ctc aag ggt cac gcg cta gct gtg aga aag att　2081
Leu His His Ala Ser Leu Lys Gly His Ala Leu Ala Val Arg Lys Ile
　　　　　　　650　　　　　　　　　655　　　　　　　　　660

ctg gct cgg gcg cgg cag ctg gtg gac gcc aag aag gag gac ggc ttc　2129
Leu Ala Arg Ala Arg Gln Leu Val Asp Ala Lys Lys Glu Asp Gly Phe
　　　665　　　　　　　　　670　　　　　　　　　675

acg gcg ctg cat ctg gct gcc ctc aac aac cac cgc gag gtg gcc cag　2177
Thr Ala Leu His Leu Ala Ala Leu Asn Asn His Arg Glu Val Ala Gln
680　　　　　　　　　685　　　　　　　　　690　　　　　　　　　695

atc ctc atc cgg gag ggc cgc tgt gac gtg aac gtg cgc aac cgg aag　2225
Ile Leu Ile Arg Glu Gly Arg Cys Asp Val Asn Val Arg Asn Arg Lys
　　　　　　　700　　　　　　　　　705　　　　　　　　　710

ctg cag tcc ccg ctg cat ctc gcc gtg caa cag gcc cac gtg ggg ctg　2273
Leu Gln Ser Pro Leu His Leu Ala Val Gln Gln Ala His Val Gly Leu
　　　　　　　715　　　　　　　　　720　　　　　　　　　725

gtg ccg cta ctg gtg gac gct ggg tgc agt gtc aac gcc gag gac gag　2321
Val Pro Leu Leu Val Asp Ala Gly Cys Ser Val Asn Ala Glu Asp Glu
　　　　　　　730　　　　　　　　　735　　　　　　　　　740

```
gag ggg gac aca gcc ctg cac gtg gcg ctg cag cgt cat cag ctg ctg    2369
Glu Gly Asp Thr Ala Leu His Val Ala Leu Gln Arg His Gln Leu Leu
    745             750             755


ccc ctg gtg gct gat ggg gcc ggg ggg gac cca ggg ccc ttg cag ctg    2417
Pro Leu Val Ala Asp Gly Ala Gly Gly Asp Pro Gly Pro Leu Gln Leu
760             765             770             775


ctg tcc agg cta cag gcc tcg ggc ctc ccc ggc agc gcg gag ctg acg    2465
Leu Ser Arg Leu Gln Ala Ser Gly Leu Pro Gly Ser Ala Glu Leu Thr
            780             785             790


gtg ggc gcg gcg gtc gcc tgc ttc ctg gcg ctg gag ggc gcc gac gtg    2513
Val Gly Ala Ala Val Ala Cys Phe Leu Ala Leu Glu Gly Ala Asp Val
            795             800             805


agc tac acc aac cac cgc ggt cgg agc ccg ctg gac ctg gcc gcc gag    2561
Ser Tyr Thr Asn His Arg Gly Arg Ser Pro Leu Asp Leu Ala Ala Glu
        810             815             820


ggt cgc gtg ctc aag gcc ctt cag ggc tgc gcc cag cgc ttc cgg gag    2609
Gly Arg Val Leu Lys Ala Leu Gln Gly Cys Ala Gln Arg Phe Arg Glu
    825             830             835


cgg cag gcg ggc ggg ggc gcg gcc ccg ggc ccc agg caa acg ctc ggg    2657
Arg Gln Ala Gly Gly Gly Ala Ala Pro Gly Pro Arg Gln Thr Leu Gly
840             845             850             855


acc ccc aac acc gtg acg aac ctg cac gtg ggc gcc gcg ccg ggg ccc    2705
```

Thr Pro Asn Thr Val Thr Asn Leu His Val Gly Ala Ala Pro Gly Pro
          860   865   870

gag gcc gct gag tgc ctg gtg tgc tcc gag ctg gcg ctg ctg gtg ctg   2753
Glu Ala Ala Glu Cys Leu Val Cys Ser Glu Leu Ala Leu Leu Val Leu
          875   880   885

ttc tcg ccg tgc cag cac cgc acc gtg tgt gag gag tgc gcg cgc agg   2801
Phe Ser Pro Cys Gln His Arg Thr Val Cys Glu Glu Cys Ala Arg Arg
          890   895   900

atg aag aag tgc atc agg tgc cag gtg gtc gtc agc aag aaa ctg cgc   2849
Met Lys Lys Cys Ile Arg Cys Gln Val Val Val Ser Lys Lys Leu Arg
  905   910   915

cca gac ggc tct gag gtg gcg agc gcc gcc ccc gcc ccc ggc ccg ccg   2897
Pro Asp Gly Ser Glu Val Ala Ser Ala Ala Pro Ala Pro Gly Pro Pro
  920   925   930   935

cgc cag ctg gtg gag gag ctg cag agc cgc tac cgg cag atg gag gaa   2945
Arg Gln Leu Val Glu Glu Leu Gln Ser Arg Tyr Arg Gln Met Glu Glu
          940   945   950

cgc atc acc tgc ccc atc tgc atc gac agc cac atc cgc ctc gtg ttc   2993
Arg Ile Thr Cys Pro Ile Cys Ile Asp Ser His Ile Arg Leu Val Phe
          955   960   965

cag tgc ggc cac ggc gca tgc gcc ccc tgc ggc tcc gcg ctc agc gcc   3041
Gln Cys Gly His Gly Ala Cys Ala Pro Cys Gly Ser Ala Leu Ser Ala

```
        970                975                 980

tgc ccc atc tgc cgc cag ccc atc cgc gac cgc atc cag atc ttc gtg    3089
Cys Pro Ile Cys Arg Gln Pro Ile Arg Asp Arg Ile Gln Ile Phe Val
        985                990                 995


tgagccgcgc cgtccgccgc gcccgagctg ccttcgcgtg cccccgccct gtgttttata 3149


aaaagaaaga ttctcggat                                               3168
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<210> 162

<211> 999

<212> PRT

<213> Homo sapiens

<400> 162

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Met Gly Trp Lys Pro Ser Glu Ala Arg Gly Gln Ser Gln Ser Leu Gln
1                5                   10                  15


Ala Ser Gly Leu Gln Pro Arg Ser Leu Lys Ala Ala Arg Arg Ala Thr
              20                 25                  30


Gly Arg Pro Asp Arg Ser Arg Ala Ala Pro Pro Asn Met Asp Pro Asp
              35                 40                  45


Pro Gln Ala Gly Val Gln Val Gly Met Arg Val Val Arg Gly Val Asp
              50                 55                  60
```

Trp Lys Trp Gly Gln Gln Asp Gly Gly Glu Gly Gly Val Gly Thr Val
65   70   75   80

Val Glu Leu Gly Arg His Gly Ser Pro Ser Thr Pro Asp Arg Thr Val
                85   90   95

Val Val Gln Trp Asp Gln Gly Thr Arg Thr Asn Tyr Arg Ala Gly Tyr
            100   105   110

Gln Gly Ala His Asp Leu Leu Leu Tyr Asp Asn Ala Gln Ile Gly Val
        115   120   125

Arg His Pro Asn Ile Ile Cys Asp Cys Cys Lys Lys His Gly Leu Arg
        130   135   140

Gly Met Arg Trp Lys Cys Arg Val Cys Leu Asp Tyr Asp Leu Cys Thr
145   150   155   160

Gln Cys Tyr Met His Asn Lys His Glu Leu Ala His Ala Phe Asp Arg
                165   170   175

Tyr Glu Thr Ala His Ser Arg Pro Val Thr Leu Ser Pro Arg Gln Gly
        180   185   190

Leu Pro Arg Ile Pro Leu Arg Gly Ile Phe Gln Gly Ala Lys Val Val
        195   200   205

Arg Gly Pro Phe Trp Glu Trp Gly Ser Gln Asp Gly Gly Glu Gly Lys
        210   215   220

Pro Gly Arg Val Val Asp Ile Arg Gly Trp Asp Val Glu Thr Gly Arg
225   230   235   240

Ser Val Ala Ser Val Thr Trp Ala Asp Gly Thr Thr Asn Val Tyr Arg
            245   250   255

Val Gly His Lys Gly Lys Val Asp Leu Lys Cys Val Gly Glu Ala Ala
            260   265   270

Gly Gly Phe Tyr Tyr Lys Asp His Leu Pro Arg Leu Gly Lys Pro Ala
            275   280   285

Glu Leu Gln Arg Arg Val Ser Ala Asp Ser Gln Pro Phe Gln His Gly
            290   295   300

Asp Lys Val Lys Cys Leu Leu Asp Thr Asp Val Leu Arg Glu Met Gln
305   310   315   320

Glu Gly His Gly Gly Trp Asn Pro Arg Met Ala Glu Phe Ile Gly Gln
            325   330   335

Thr Gly Thr Val His Arg Ile Thr Asp Arg Gly Asp Val Arg Val Gln
            340   345   350

Phe Asn His Glu Thr Arg Trp Thr Phe His Pro Gly Ala Leu Thr Lys
            355   360   365

His His Ser Phe Trp Val Gly Asp Val Val Arg Val Ile Gly Asp Leu

370   375   380

Asp Thr Val Lys Arg Leu Gln Ala Gly His Gly Glu Trp Thr Asp Asp
385   390   395   400

Met Ala Pro Ala Leu Gly Arg Val Gly Lys Val Val Lys Val Phe Gly
              405   410   415

Asp Gly Asn Leu Arg Val Ala Val Ala Gly Gln Arg Trp Thr Phe Ser
              420   425   430

Pro Ser Cys Leu Val Ala Tyr Arg Pro Glu Glu Asp Ala Asn Leu Asp
              435   440   445

Val Ala Glu Arg Ala Arg Glu Asn Lys Ser Ser Leu Ser Val Ala Leu
         450   455   460

Asp Lys Leu Arg Ala Gln Lys Ser Asp Pro Glu His Pro Gly Arg Leu
465   470   475   480

Val Val Glu Val Ala Leu Gly Asn Ala Ala Arg Ala Leu Asp Leu Leu
              485   490   495

Arg Arg Arg Pro Glu Gln Val Asp Thr Lys Asn Gln Gly Arg Thr Ala
              500   505   510

Leu Gln Val Ala Ala Tyr Leu Gly Gln Val Glu Leu Ile Arg Leu Leu
              515   520   525

Leu Gln Ala Arg Ala Gly Val Asp Leu Pro Asp Asp Glu Gly Asn Thr
530   535   540

Ala Leu His Tyr Ala Ala Leu Gly Asn Gln Pro Glu Ala Thr Arg Val
545   550   555   560

Leu Leu Ser Ala Gly Cys Arg Ala Asp Ala Ile Asn Ser Thr Gln Ser
565   570   575

Thr Ala Leu His Val Ala Val Gln Arg Gly Phe Leu Glu Val Val Arg
580   585   590

Ala Leu Cys Glu Arg Gly Cys Asp Val Asn Leu Pro Asp Ala His Ser
595   600   605

Asp Thr Pro Leu His Ser Ala Ile Ser Ala Gly Thr Gly Ala Ser Gly
610   615   620

Ile Val Glu Val Leu Thr Glu Val Pro Asn Ile Asp Val Thr Ala Thr
625   630   635   640

Asn Ser Gln Gly Phe Thr Leu Leu His His Ala Ser Leu Lys Gly His
645   650   655

Ala Leu Ala Val Arg Lys Ile Leu Ala Arg Ala Arg Gln Leu Val Asp
660   665   670

Ala Lys Lys Glu Asp Gly Phe Thr Ala Leu His Leu Ala Ala Leu Asn
675   680   685

Asn His Arg Glu Val Ala Gln Ile Leu Ile Arg Glu Gly Arg Cys Asp
   690   695   700

Val Asn Val Arg Asn Arg Lys Leu Gln Ser Pro Leu His Leu Ala Val
   705   710   715   720

Gln Gln Ala His Val Gly Leu Val Pro Leu Leu Val Asp Ala Gly Cys
            725   730   735

Ser Val Asn Ala Glu Asp Glu Glu Gly Asp Thr Ala Leu His Val Ala
         740   745   750

Leu Gln Arg His Gln Leu Leu Pro Leu Val Ala Asp Gly Ala Gly Gly
      755   760   765

Asp Pro Gly Pro Leu Gln Leu Leu Ser Arg Leu Gln Ala Ser Gly Leu
   770   775   780

Pro Gly Ser Ala Glu Leu Thr Val Gly Ala Ala Val Ala Cys Phe Leu
   785   790   795   800

Ala Leu Glu Gly Ala Asp Val Ser Tyr Thr Asn His Arg Gly Arg Ser
         805   810   815

Pro Leu Asp Leu Ala Ala Glu Gly Arg Val Leu Lys Ala Leu Gln Gly
         820   825   830

Cys Ala Gln Arg Phe Arg Glu Arg Gln Ala Gly Gly Gly Ala Ala Pro

                835   840   845

Gly Pro Arg Gln Thr Leu Gly Thr Pro Asn Thr Val Thr Asn Leu His
      850   855   860

Val Gly Ala Ala Pro Gly Pro Glu Ala Ala Glu Cys Leu Val Cys Ser
      865   870   875   880

Glu Leu Ala Leu Leu Val Leu Phe Ser Pro Cys Gln His Arg Thr Val
                      885   890   895

Cys Glu Glu Cys Ala Arg Arg Met Lys Lys Cys Ile Arg Cys Gln Val
                      900   905   910

Val Val Ser Lys Lys Leu Arg Pro Asp Gly Ser Glu Val Ala Ser Ala
                      915   920   925

Ala Pro Ala Pro Gly Pro Pro Arg Gln Leu Val Glu Glu Leu Gln Ser
            930   935   940

Arg Tyr Arg Gln Met Glu Glu Arg Ile Thr Cys Pro Ile Cys Ile Asp
945   950   955   960

Ser His Ile Arg Leu Val Phe Gln Cys Gly His Gly Ala Cys Ala Pro
                      965   970   975

Cys Gly Ser Ala Leu Ser Ala Cys Pro Ile Cys Arg Gln Pro Ile Arg
                      980   985   990

Asp Arg Ile Gln Ile Phe Val
      995

<210> 163

<211> 4031

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(2649)

<400> 163

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tcccgtcgcc aatccccgcc gtcccgggcc atg atc gcc tgg cgt ctg ccc ttg 114
                                              Met Ile Ala Trp Arg Leu Pro Leu
                                          1   5

tgc gtg ctc ttg gtg gcc tcc gtc gag agc cac ctg ggg gcc ctg ggg 162
Cys Val Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Ala Leu Gly
    10   15   20

ccc aag aac gtc tcg cag aaa gac gcg gag ttt gag cgc acc tac gcg 210
Pro Lys Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Ala
 25   30   35   40

gac gac gtc aac agc gag ctg gtc aac atc tac acc ttc aac cac acc   258
Asp Asp Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr
              45   50   55

gtg acc cgc aac cgg acc gag ggt gtg cga gtg tct gtg aat gtc ctg   306
Val Thr Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu
              60   65   70

aac aag cag aaa ggg gcg cct ttg ctg ttc gtg gtc cgc cag aag gag   354
Asn Lys Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu
              75   80   85

gct gtt gtg tcc ttc cag gtg ccc cta atc ctt cga gga ctg tat cag   402
Ala Val Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Leu Tyr Gln
              90   95   100

cgg aag tac ctc tac caa aaa gtg gaa cga act ctg tgt cag ccc ccc   450
Arg Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
105   110   115   120

acc aag aat gag tct gag atc cag ttt ttc tat gtg gac gtg tct acc   498
Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr
              125   130   135

ctg tca ccc gtc aat acc act tac cag ctc cga gtc aac cgt gtg gac   546
Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Asn Arg Val Asp
              140   145   150

aat ttt gtg ctc agg act gga gag ctg ttt acc ttt aat acc act gca   594

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        Asn Phe Val Leu Arg Thr Gly Glu Leu Phe Thr Phe Asn Thr Thr Ala
                155                 160                 165


        gcc cag ccc cag tac ttc aaa tac gag ttt cct gat ggt gtg gac tcg    642
        Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Asp Gly Val Asp Ser
                170                 175                 180


        gta att gtc aag gtg acc tcc aag aag gcc ttc ccc tgc tca gtc atc    690
        Val Ile Val Lys Val Thr Ser Lys Lys Ala Phe Pro Cys Ser Val Ile
                185                 190                 195                 200


        tcc atc cag gat gtc ctg tgc cct gtc tat gat ctg gac aac agt gta    738
        Ser Ile Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Ser Val
                        205                 210                 215


        gcc ttc att ggc atg tac cag acg atg act aag aag gca gcc atc act    786
        Ala Phe Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr
                        220                 225                 230


        gtg cag cgg aaa gac ttc ccc agc aac agc ttc tat gtg gtg gtg gta    834
        Val Gln Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val
                        235                 240                 245


        gtg aag act gag gac cag gcc tgc gga ggg tcc ttg ccc ttc tac cct    882
        Val Lys Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro
                250                 255                 260


        ttt gtg gaa gat gag cca gtg gat caa ggg cac cgt cag aaa aca ctg    930
        Phe Val Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu
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265   270   275   280

tca gtg ctg gtc tct cag gct gtc aca tct gag gcc tat gtt ggt ggg   978
Ser Val Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Gly Gly
            285   290   295

atg ctc ttt tgc ctg ggc ata ttc ttg tcc ttc tac ctg ctg act gtg   1026
Met Leu Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val
            300   305   310

ctg ctg gcc tgt tgg gag aac tgg agg caa agg aag aag acc ttg ctg   1074
Leu Leu Ala Cys Trp Glu Asn Trp Arg Gln Arg Lys Lys Thr Leu Leu
            315   320   325

gtg gcc ata gac cga gcc tgc cca gaa agt ggt cac gct cgg gtc ttg   1122
Val Ala Ile Asp Arg Ala Cys Pro Glu Ser Gly His Ala Arg Val Leu
            330   335   340

gct gat tca ttt cct ggc agt gcc cct tac gag ggt tac aac tat ggc   1170
Ala Asp Ser Phe Pro Gly Ser Ala Pro Tyr Glu Gly Tyr Asn Tyr Gly
345   350   355   360

tcc ttt gaa aat ggt tcc gga tcc act gac ggg ttg gtt gaa agc gca   1218
Ser Phe Glu Asn Gly Ser Gly Ser Thr Asp Gly Leu Val Glu Ser Ala
            365   370   375

ggt tca ggg gac ctc tcc tac agt tac cag ggg cac gac cag ttc aag   1266
Gly Ser Gly Asp Leu Ser Tyr Ser Tyr Gln Gly His Asp Gln Phe Lys
            380   385   390

cgg cgc ctt ccc tct ggc cag atg cgg cag ctg tgc att gcc atg gac   1314
Arg Arg Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Asp
      395   400   405

cgc tcc ttt gac gca gtg ggt cct cgg cct cga ctg gac tcc atg agc   1362
Arg Ser Phe Asp Ala Val Gly Pro Arg Pro Arg Leu Asp Ser Met Ser
      410   415   420

tcc gtg gaa gag gat gac tac gac acg ctg act gac atc gac tca gac   1410
Ser Val Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp
425   430   435   440

aaa aac gtc att cga acc aag caa tac ctc tgt gtg gct gat ctg gca   1458
Lys Asn Val Ile Arg Thr Lys Gln Tyr Leu Cys Val Ala Asp Leu Ala
            445   450   455

cga aag gac aaa cgt gtt ttg cgg aaa aag tac cag att tac ttc tgg   1506
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp
            460   465   470

aac ata gcc acc att gcg gtc ttc tac gca ctt cct gtg gtg cag ctg   1554
Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu
      475   480   485

gtg atc acc tac cag acg gtg gtg aat gtc aca ggg aac cag gac atc   1602
Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile
      490   495   500

tgc tac tac aac ttc ctc tgt gcc cac ccg ctg ggc aac ctc agc gcc   1650
Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala
505   510   515   520

ttc aac aac atc ctc agc aac ttg ggg tac atc ctg ctg ggg ctg ctc   1698
Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu
                 525   530   535

ttc ctg ctc atc atc ctg cag cga gag atc aat cat aac cgg gcc ctg   1746
Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu
                 540   545   550

ctg cgg aat gac ctc tat gct ctg gag tgt ggg atc ccc aaa cac ttt   1794
Leu Arg Asn Asp Leu Tyr Ala Leu Glu Cys Gly Ile Pro Lys His Phe
                 555   560   565

ggt ctg ttt tac gcc atg ggc aca gca ctg atg atg gag ggg cta ctt   1842
Gly Leu Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu
             570   575   580

agt gcc tgt tac cac gtc tgc ccc aac tac acc aac ttc cag ttt gat   1890
Ser Ala Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp
585   590   595   600

acc tcc ttc atg tac atg att gct ggc ctc tgc atg ctg aag ctc tac   1938
Thr Ser Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr
                 605   610   615

cag aag cgg cac cca gat atc aac gcc agt gcc tac agt gca tat gcc   1986

Gln Lys Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala
      620   625   630

tgc ttg gcc atc gtc atc ttc ttc tcc gtt ctg ggc gtg gtg ttt ggc   2034
Cys Leu Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly
      635   640   645

aaa ggg aac acg gcc ttc tgg att gtc ttc tcc gtc att cac atc atc   2082
Lys Gly Asn Thr Ala Phe Trp Ile Val Phe Ser Val Ile His Ile Ile
      650   655   660

tcc acc ctg ctc ctc agc act cag ctc tat tac atg ggc cgc tgg aag   2130
Ser Thr Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys
665   670   675   680

ctg gac ttc ggg atc ttc cgc cgc atc ctc cat gtg ctc tac aca gac   2178
Leu Asp Phe Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
           685   690   695

tgc atc cgg cag tgc agc ggg ccc ctt tac acg gac cgc atg gtg ctt   2226
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Thr Asp Arg Met Val Leu
      700   705   710

ctg gtc atg ggc aac att atc aac tgg tcg ctg gct gca tac gga ctc   2274
Leu Val Met Gly Asn Ile Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu
      715   720   725

atc atg cgc ccc aat gac ttt gct tcc tac ttg ctg gca att ggc atc   2322
Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile

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             730                    735                    740

tgc aac ctg ctg ctt tat ttc gcc ttc tac atc atc atg aag ctc cgg   2370
Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg
745                    750                    755                    760


agc ggc gag agg atc aag ctc atc cct ctg ctt tgc atc gtc tgc acc   2418
Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr
                   765                    770                    775


tcc gtg gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctg agc   2466
Ser Val Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser
                   780                    785                    790


acg tgg cag aaa acc ccc gca gag tcc agg gag cac aac cgc gac tgc   2514
Thr Trp Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys
                   795                    800                    805


atc ctc ctc gac ttc ttt gat gac cac gat atc tgg cac ttc ctg tcc   2562
Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser
                   810                    815                    820


tcc att gcc atg ttt ggg tcc ttc ctg gtt ttg ctg acg ttg gat gac   2610
Ser Ile Ala Met Phe Gly Ser Phe Leu Val Leu Leu Thr Leu Asp Asp
825                    830                    835                    840


gac ttg gac aca gta cag cgg gac aag atc tat gtc ttc tagcagcatc   2659
Asp Leu Asp Thr Val Gln Arg Asp Lys Ile Tyr Val Phe
                   845                    850
```

出証特２００２－３０３２９３５

tgtggtccag gcttcacctc acgggcctag cgcctgcctc tgcatcacct gccagttgcc 2719

acaagaacac cacgggtgtg agtcccagct ctgctgccca gcattggatg tcgtggcaag 2779

acagcgagat tccagcccag gcctgactca ggacagttcc tggtggcact gagccttgga 2839

gttgcctctg cggaggagga ggcctgctcc gcattcccca gacactggcc aaattgctgc 2899

tttcttctca gtgttgggtc ctccccagga ccctagtctg tccatctgtc ttgtttatcc 2959

actggctctc catttgtccc tttggagagg aaggtgggaa ggcaatgtcc tgtcccattt 3019

catgccttgc attctgccca tcccttccct cctctcagct taggacacac agccctttct 3079

tcttcccatg ctctgtccag gaccacagtc tggtgcctga ttctttgtcc atcaccagga 3139

cctaagctct ccctgggtct gtagctggct gctatcactg cccactctga cctgccagga 3199

cagatgcagg taggagactt tgggggctgg ccagctggtg ccaggctttc ggtgctaagg 3259

cctggaaggg gcctaggtac gaccctcctc cctgacctgt gcttggagct ggctcttcag 3319

cagtgagggc cagcccaagt tgagtcttct gatcggggac tgaattcaga ggccacctca 3379

tcccaccagc cactagaatg atgccagcac tagggttggt gggaagtggc aactcactgt 3439

ccccttccac accctcagtc ctgccaagcc ccagatgggg gcctctcagt gccattgaca 3499

ctgcccaaga atgtctagag gccacggaac ggtgccaagc acacagtccc ttttgcctct 3559

ttcacgggag caggagtccc agtgcctgtc gtggaaaggg aggaacatgc caggtccctg 3619

tgtgtccttg gccctgtctc accaaaggac tcagggctgg tttctgagtt tccgtccagt 3679

atttagccaa gttctgtgtt agtcacgtag gcctaagagc cttggcgttt acagagtcac 3739

ccagctctgg cccctggcca ttctggtcct tggcgtttac agagtcaccc agctccaggc 3799

ccctggccac tttggtactt ggttgccctt cacttcacca ggtccattcc agatgccaag 3859

agtgggcccc aggaatgtgt ttccttctct ccaccatgtt tttatagctc ttgggctggg 3919

agaagaggcg ggtctgggtc tttgtttctg agctttgttc tatgttcctc catgctacgg 3979

ttgcaattgt tttctatgaa cgagtacatt caataaagac aaccagacct gg 4031

<210> 164

<211> 853

<212> PRT

<213> Homo sapiens

<400> 164

Met Ile Ala Trp Arg Leu Pro Leu Cys Val Leu Leu Val Ala Ser Val
1   5   10   15

Glu Ser His Leu Gly Ala Leu Gly Pro Lys Asn Val Ser Gln Lys Asp

```
                20                    25                    30

Ala Glu Phe Glu Arg Thr Tyr Ala Asp Asp Val Asn Ser Glu Leu Val
            35                    40                    45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
        50                    55                    60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
    65                    70                    75                    80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85                    90                    95

Leu Ile Leu Arg Gly Leu Tyr Gln Arg Lys Tyr Leu Tyr Gln Lys Val
                100                   105                   110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
            115                   120                   125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
        130                   135                   140

Gln Leu Arg Val Asn Arg Val Asp Asn Phe Val Leu Arg Thr Gly Glu
145                   150                   155                   160

Leu Phe Thr Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
                165                   170                   175
```

```
Glu Phe Pro Asp Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Lys
            180                 185                 190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
            195                 200                 205

Val Tyr Asp Leu Asp Asn Ser Val Ala Phe Ile Gly Met Tyr Gln Thr
            210                 215                 220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225                 230                 235                 240

Asn Ser Phe Tyr Val Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
                    245                 250                 255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Val Glu Asp Glu Pro Val Asp
            260                 265                 270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
            275                 280                 285

Thr Ser Glu Ala Tyr Val Gly Gly Met Leu Phe Cys Leu Gly Ile Phe
            290                 295                 300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305                 310                 315                 320

Arg Gln Arg Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
            325                 330                 335
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出証特２００２－３０３２９３５

Glu Ser Gly His Ala Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ala
          340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Gly Ser Gly Ser
          355   360   365

Thr Asp Gly Leu Val Glu Ser Ala Gly Ser Gly Asp Leu Ser Tyr Ser
          370   375   380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Asp Arg Ser Phe Asp Ala Val Gly Pro
             405   410   415

Arg Pro Arg Leu Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
          420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln
          435   440   445

Tyr Leu Cys Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
          450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val

```
                   485                490                495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
              500                505                510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
              515                520                525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
              530                535                540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Tyr Ala Leu
545                550                555                560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
                   565                570                575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
              580                585                590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
              595                600                605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
              610                615                620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
625                630                635                640
```

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
              645   650   655

Val Phe Ser Val Ile His Ile Ile Ser Thr Leu Leu Leu Ser Thr Gln
              660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Phe Gly Ile Phe Arg Arg
              675   680   685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
            690   695   700

Leu Tyr Thr Asp Arg Met Val Leu Leu Val Met Gly Asn Ile Ile Asn
705   710   715   720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
              725   730   735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
              740   745   750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
              755   760   765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
            770   775   780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785   790   795   800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
        805   810   815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
        820   825   830

Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln Arg Asp
        835   840   845

Lys Ile Tyr Val Phe
        850

<210> 165

<211> 3138

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)..(2648)

<400> 165

gccgcaaccc gtcccggagg tgtcctgtct cctgtcgccg ccgccgccgc caccaccgct 60

gccactgccg ccctgccggg gcc atg ttc gct ctg ggc ttg ccc ttc ttg gtg 113
                         Met Phe Ala Leu Gly Leu Pro Phe Leu Val

```
                    1                5                        10

ctc ttg gtg gcc tcg gtc gag agc cat ctg ggg gtt ctg ggg ccc aag   161
Leu Leu Val Ala Ser Val Glu Ser His Leu Gly Val Leu Gly Pro Lys
             15              20                  25


aac gtc tcg cag aaa gac gcc gag ttt gag cgc acc tac gtg gac gag   209
Asn Val Ser Gln Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu
             30              35                  40


gtc aac agc gag ctg gtc aac atc tac acc ttc aac cat act gtg acc   257
Val Asn Ser Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr
             45              50                  55


cgc aac agg aca gag ggc gtg cgt gtg tct gtg aac gtc ctg aac aag   305
Arg Asn Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys
          60              65                  70


cag aag ggg gcg ccg ttg ctg ttt gtg gtc cgc cag aag gag gct gtg   353
Gln Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
75              80                  85                  90


gtg tcc ttc cag gtg ccc cta atc ctg cga ggg atg ttt cag cgc aag   401
Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg Lys
             95              100                 105


tac ctc tac caa aaa gtg gaa cga acc ctg tgt cag ccc ccc acc aag   449
Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys
             110             115                 120
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aat gag tcg gag att cag ttc ttc tac gtg gat gtg tcc acc ctg tca    497
Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser Thr Leu Ser
        125             130             135


cca gtc aac acc aca tac cag ctc cgg gtc agc cgc atg gac gat ttt    545
Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg Met Asp Asp Phe
        140             145             150


gtg ctc agg act ggg gag cag ttc agc ttc aat acc aca gca gca cag    593
Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln
155             160             165             170


ccc cag tac ttc aag tat gag ttc cct gaa ggc gtg gac tcg gta att    641
Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu Gly Val Asp Ser Val Ile
                175             180             185


gtc aag gtg acc tcc aac aag gcc ttc ccc tgc tca gtc atc tcc att    689
Val Lys Val Thr Ser Asn Lys Ala Phe Pro Cys Ser Val Ile Ser Ile
            190             195             200


cag gat gtg ctg tgt cct gtc tat gac ctg gac aac aac gta gcc ttc    737
Gln Asp Val Leu Cys Pro Val Tyr Asp Leu Asp Asn Asn Val Ala Phe
        205             210             215


atc ggc atg tac cag acg atg acc aag aag gcg gcc atc acc gta cag    785
Ile Gly Met Tyr Gln Thr Met Thr Lys Lys Ala Ala Ile Thr Val Gln
        220             225             230
```

cgc aaa gac ttc ccc agc aac agc ttt tat gtg gtg gtg gtg gtg aag   833
Arg Lys Asp Phe Pro Ser Asn Ser Phe Tyr Val Val Val Val Val Lys
235   240   245   250

acc gaa gac caa gcc tgc ggg ggc tcc ctg cct ttc tac ccc ttc gca   881
Thr Glu Asp Gln Ala Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala
        255   260   265

gaa gat gaa ccg gtc gat caa ggg cac cgc cag aaa acc ctg tca gtg   929
Glu Asp Glu Pro Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val
        270   275   280

ctg gtg tct caa gca gtc acg tct gag gca tac gtc agt ggg atg ctc   977
Leu Val Ser Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu
        285   290   295

ttt tgc ctg ggt ata ttt ctc tcc ttt tac ctg ctg acc gtc ctc ctg   1025
Phe Cys Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu
        300   305   310

gcc tgc tgg gag aac tgg agg cag aag aag aag acc ctg ctg gtg gcc   1073
Ala Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala
315   320   325   330

att gac cga gcc tgc cca gaa agc ggt cac cct cga gtc ctg gct gat   1121
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala Asp
        335   340   345

tct ttt cct ggc agt tcc cct tat gag ggt tac aac tat ggc tcc ttt   1169

Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe
                350   355   360

gag aat gtt tct gga tct acc gat ggt ctg gtt gac agc gct ggc act   1217
Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser Ala Gly Thr
                365   370   375

ggg gac ctc tct tac ggt tac cag ggg cac gac cag ttc aag cgg cgc   1265
Gly Asp Leu Ser Tyr Gly Tyr Gln Gly His Asp Gln Phe Lys Arg Arg
                380   385   390

ctc ccc tct ggc cag atg cgg cag ctg tgc att gcc atg ggc cgc tcc   1313
Leu Pro Ser Gly Gln Met Arg Gln Leu Cys Ile Ala Met Gly Arg Ser
395   400   405   410

ttt gaa cct gta ggt act cgg ccc cga gtg gac tcc atg agc tct gtg   1361
Phe Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val
                415   420   425

gag gag gat gac tac gac aca ttg acc gac atc gat tcc gac aag aat   1409
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn
                430   435   440

gtc att cgc acc aag caa tac ctc tat gtg gct gac ctg gca cgg aag   1457
Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys
                445   450   455

gac aag cgt gtt ctg cgg aaa aag tac cag atc tac ttc tgg aac att   1505
Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile

460 465 470

```
gcc acc att gct gtc ttc tat gcc ctt cct gtg gtg cag ctg gtg atc    1553
Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val Gln Leu Val Ile
475         480         485         490


acc tac cag acg gtg gtg aat gtc aca ggg aat cag gac atc tgc tac    1601
Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr
          495         500         505


tac aac ttc ctc tgc gcc cac cca ctg ggc aat ctc agc gcc ttc aac    1649
Tyr Asn Phe Leu Cys Ala His Pro Leu Gly Asn Leu Ser Ala Phe Asn
          510         515         520


aac atc ctc agc aac ctg ggg tac atc ctg ctg ggg ctg ctt ttc ctg    1697
Asn Ile Leu Ser Asn Leu Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu
          525         530         535


ctc atc atc ctg caa cgg gag atc aac cac aac cgg gcc ctg ctg cgc    1745
Leu Ile Ile Leu Gln Arg Glu Ile Asn His Asn Arg Ala Leu Leu Arg
          540         545         550


aat gac ctc tgt gcc ctg gaa tgt ggg atc ccc aaa cac ttt ggg ctt    1793
Asn Asp Leu Cys Ala Leu Glu Cys Gly Ile Pro Lys His Phe Gly Leu
555         560         565         570


ttc tac gcc atg ggc aca gcc ctg atg atg gag ggg ctg ctc agt gct    1841
Phe Tyr Ala Met Gly Thr Ala Leu Met Met Glu Gly Leu Leu Ser Ala
          575         580         585
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tgc tat cat gtg tgc ccc aac tat acc aat ttc cag ttt gac aca tcg   1889
Cys Tyr His Val Cys Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser
            590   595   600

ttc atg tac atg atc gcc gga ctc tgc atg ctg aag ctc tac cag aag   1937
Phe Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys
            605   610   615

cgg cac ccg gac atc aac gcc agc gcc tac agt gcc tac gcc tgc ctg   1985
Arg His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu
         620   625   630

gcc att gtc atc ttc ttc tct gtg ctg ggc gtg gtc ttt ggc aaa ggg   2033
Ala Ile Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly
635   640   645   650

aac acg gcg ttc tgg atc gtc ttc tcc atc att cac atc atc gcc acc   2081
Asn Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
            655   660   665

ctg ctc ctc agc acg cag ctc tat tac atg ggc cgg tgg aaa ctg gac   2129
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp
            670   675   680

tcg ggg atc ttc cgc cgc atc ctc cac gtg ctc tac aca gac tgc atc   2177
Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp Cys Ile
            685   690   695

```
cgg cag tgc agc ggg ccg ctc tac gtg gac cgc atg gtg ctg ctg gtc        2225
Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val Leu Leu Val
    700             705             710


atg ggc aac gtc atc aac tgg tcg ctg gct gcc tat ggg ctt atc atg        2273
Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met
    715             720             725             730


cgc ccc aat gat ttc gct tcc tac ttg ttg gcc att ggc atc tgc aac        2321
Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn
                    735             740             745


ctg ctc ctt tac ttc gcc ttc tac atc atc atg aag ctc cgg agt ggg        2369
Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly
                750             755             760


gag agg atc aag ctc atc ccc ctg ctc tgc atc gtt tgc acc tcc gtg        2417
Glu Arg Ile Lys Leu Ile Pro Leu Leu Cys Ile Val Cys Thr Ser Val
            765             770             775


gtc tgg ggc ttc gcg ctc ttc ttc ttc ttc cag gga ctc agc acc tgg        2465
Val Trp Gly Phe Ala Leu Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp
    780             785             790


cag aaa acc cct gca gag tcg agg gag cac aac cgg gac tgc atc ctc        2513
Gln Lys Thr Pro Ala Glu Ser Arg Glu His Asn Arg Asp Cys Ile Leu
    795             800             805             810


ctc gac ttc ttt gac gac cac gac atc tgg cac ttc ctc tcc tcc atc        2561
```

```
Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe Leu Ser Ser Ile
              815                 820                 825


gcc atg ttc ggg tcc ttc ctg gta agc ggg cct ccc ggc cga gcc ggg    2609
Ala Met Phe Gly Ser Phe Leu Val Ser Gly Pro Pro Gly Arg Ala Gly
              830                 835                 840


tgg gta cgt gaa ggt agc agc tgc ctc ctt ccc tgt ggc tgatctggcg     2658
Trp Val Arg Glu Gly Ser Ser Cys Leu Leu Pro Cys Gly
          845                 850                 855
```

tccacacccc aggtgttgct gacactggat gacgacctgg atacttagaa aggggcttca 2718

ggaagggatg tgctgtttcc ctctacgtgc ccagtcctag cctcgctcta ggacccaggg 2778

ctggcttcta agtttccgtc cagtcttcag gcaagttctg tgttagtcat gcacacacat 2838

acctatgaaa ccttggagtt tacaaagaat tgccccagct ctgggcaccc tggccaccct 2898

ggtccttgga tccccttcgt cccacctggt ccaccccaga tgctgaggat gggggagctc 2958

aggcggggcc tctgctttgg ggatgggaat gtgttttct cccaaacttg ttttatagc 3018

tctgcttgaa gggctgggag atgaggtggg tctggatctt ttctcagagc gtctccatgc 3078

tatggttgca tttccgtttt ctatgaatga atttgcattc aataaacaac cagactcagt 3138

<210> 166

<211> 855

<212> PRT

<213> Homo sapiens

<400> 166

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser Val
1   5   10   15

Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln Lys Asp
                20   25   30

Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser Glu Leu Val
            35   40   45

Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn Arg Thr Glu Gly
        50   55   60

Val Arg Val Ser Val Asn Val Leu Asn Lys Gln Lys Gly Ala Pro Leu
65   70   75   80

Leu Phe Val Val Arg Gln Lys Glu Ala Val Val Ser Phe Gln Val Pro
                85   90   95

Leu Ile Leu Arg Gly Met Phe Gln Arg Lys Tyr Leu Tyr Gln Lys Val
            100   105   110

Glu Arg Thr Leu Cys Gln Pro Pro Thr Lys Asn Glu Ser Glu Ile Gln
            115   120   125

Phe Phe Tyr Val Asp Val Ser Thr Leu Ser Pro Val Asn Thr Thr Tyr
          130   135   140

Gln Leu Arg Val Ser Arg Met Asp Asp Phe Val Leu Arg Thr Gly Glu
145   150   155   160

Gln Phe Ser Phe Asn Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr
                165   170   175

Glu Phe Pro Glu Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn
                180   185   190

Lys Ala Phe Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro
                195   200   205

Val Tyr Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr
          210   215   220

Met Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
225   230   235   240

Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala Cys
                245   250   255

Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro Val Asp
                260   265   270

Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser Gln Ala Val
          275   280   285

Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys Leu Gly Ile Phe
    290   295   300

Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala Cys Trp Glu Asn Trp
305   310   315   320

Arg Gln Lys Lys Lys Thr Leu Leu Val Ala Ile Asp Arg Ala Cys Pro
                325   330   335

Glu Ser Gly His Pro Arg Val Leu Ala Asp Ser Phe Pro Gly Ser Ser
            340   345   350

Pro Tyr Glu Gly Tyr Asn Tyr Gly Ser Phe Glu Asn Val Ser Gly Ser
        355   360   365

Thr Asp Gly Leu Val Asp Ser Ala Gly Thr Gly Asp Leu Ser Tyr Gly
    370   375   380

Tyr Gln Gly His Asp Gln Phe Lys Arg Arg Leu Pro Ser Gly Gln Met
385   390   395   400

Arg Gln Leu Cys Ile Ala Met Gly Arg Ser Phe Glu Pro Val Gly Thr
            405   410   415

Arg Pro Arg Val Asp Ser Met Ser Ser Val Glu Glu Asp Asp Tyr Asp
            420   425   430

Thr Leu Thr Asp Ile Asp Ser Asp Lys Asn Val Ile Arg Thr Lys Gln

                  435   440   445

Tyr Leu Tyr Val Ala Asp Leu Ala Arg Lys Asp Lys Arg Val Leu Arg
      450   455   460

Lys Lys Tyr Gln Ile Tyr Phe Trp Asn Ile Ala Thr Ile Ala Val Phe
  465   470   475   480

Tyr Ala Leu Pro Val Val Gln Leu Val Ile Thr Tyr Gln Thr Val Val
                  485   490   495

Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala
              500   505   510

His Pro Leu Gly Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu
          515   520   525

Gly Tyr Ile Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg
      530   535   540

Glu Ile Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu
545   550   555   560

Glu Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
                  565   570   575

Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys Pro
                  580   585   590

Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met Ile Ala
    595   600   605

Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro Asp Ile Asn
    610   615   620

Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile Val Ile Phe Phe
    625   630   635   640

Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn Thr Ala Phe Trp Ile
               645   650   655

Val Phe Ser Ile Ile His Ile Ile Ala Thr Leu Leu Leu Ser Thr Gln
               660   665   670

Leu Tyr Tyr Met Gly Arg Trp Lys Leu Asp Ser Gly Ile Phe Arg Arg
               675   680   685

Ile Leu His Val Leu Tyr Thr Asp Cys Ile Arg Gln Cys Ser Gly Pro
              690   695   700

Leu Tyr Val Asp Arg Met Val Leu Leu Val Met Gly Asn Val Ile Asn
    705   710   715   720

Trp Ser Leu Ala Ala Tyr Gly Leu Ile Met Arg Pro Asn Asp Phe Ala
               725   730   735

Ser Tyr Leu Leu Ala Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala
               740   745   750

Phe Tyr Ile Ile Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile
      755   760   765

Pro Leu Leu Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu
      770   775   780

Phe Phe Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu
785   790   795   800

Ser Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp
               805   810   815

His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser Phe
               820   825   830

Leu Val Ser Gly Pro Pro Gly Arg Ala Gly Trp Val Arg Glu Gly Ser
      835   840   845

Ser Cys Leu Leu Pro Cys Gly
      850   855

<210> 167

<211> 2815

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)..(571)

<400> 167

gcgaagcgcg cctgcgaccc ggcgtccggg cgcgctggag aggacgcgag gagcc atg   58

                                                                Met

                                                                 1

agg cgc cag cct gcg aag gtg gcg gcg ctg ctg ctc ggg ctg ctc ttg   106
Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu Leu
              5   10   15

gag tgc aca gaa gcc aaa aag cat tgc tgg tat ttc gaa gga ctc tat   154
Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu Tyr
             20   25   30

cca acc tat tat ata tgc cgc tcc tac gag gac tgc tgt ggc tcc agg   202
Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser Arg
         35   40   45

tgc tgt gtg cgg gcc ctc tcc ata cag agg ctg tgg tac ttc tgg ttc   250
Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp Phe
50   55   60   65

ctt ctg atg atg ggc gtg ctt ttc tgc tgc gga gcc ggc ttc ttc atc   298
Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe Ile
             70   75   80

```
cgg agg cgc atg tac ccc ccg ccg ctg atc gag gag cca gcc ttc aat    346
Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe Asn
         85                  90                  95
```

```
gtg tcc tac acc agg cag ccc cca aat ccc ggc cca gga gcc cag cag    394
Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln Gln
        100                 105                 110
```

```
ccg ggg ccg ccc tat tac acc gac cca gga gga ccg ggg atg aac cct    442
Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn Pro
        115                 120                 125
```

```
gtc ggg aat tcc atg gca atg gct ttc cag gtc cca ccc aac tca ccc    490
Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser Pro
130                 135                 140                 145
```

```
cag ggg agt gtg gcc tgc ccg ccc cct cca gcc tac tgc aac acg cct    538
Gln Gly Ser Val Ala Cys Pro Pro Pro Pro Ala Tyr Cys Asn Thr Pro
                150                 155                 160
```

```
ccg ccc ccg tac gaa cag gta gtg aag gcc aag tagtggggtg cccacgtgca 591
Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
                165                 170
```

```
agaggaggga caggagaggg cctttccctg gcctttctgt cttcgttgat gttcacttcc 651
```

```
aggaacggtc tcgtgggctg ctaagggcag ttcctctgat atcctcacag caagcacagc 711
```

```
tctctttcag gctttccatg gagtacaata tatgaactca cactttgtct cctctgttgc 771
```

ttctgtttct gacgcagtct gtgctctcac atggtagtgt ggtgacagtc cccgagggct 831

gacgtcctta cggtggcgtg accagatcta cgggagagag actgagagga agaaggcagt 891

gctggaggtg caggtggcat gtagaggggc caggccgagc atcccaggca agcatccttc 951

tgcccgggta ttaataggaa gccccatgcc gggcggctca gccgatgaag cagcagccga 1011

ctgagctgag cccagcaggt catctgctcc agcctgtcct ctcgtcagcc ttcctcttcc 1071

agaagctgtt ggagagacat tcaggagaga gcaagcccct tgtcatgttt ctgtctctgt 1131

tcatatccta aagatagact tctcctgcac cgccagggaa gggtagcacg tgcagctctc 1191

accgcaggat ggggcctaga atcaggcttg ccttggaggc ctgacagtga tctgacatcc 1251

actaagcaaa tttatttaaa ttcatgggaa atcacttcct gccccaaact gagacattgc 1311

attttgtgag ctcttggtct gatttggaga aaggactgtt acccattttt ttggtgtgtt 1371

tatggaagtg catgtagagc gtcctgccct ttgaaatcag actgggtgtg tgtcttccct 1431

ggacatcact gcctctccag ggcattctca ggcccggggg tctccttccc tcaggcagct 1491

ccagtggtgg gttctgaagg gtgctttcaa aacggggcac atctggctgg gaagtcacat 1551

ggactcttcc agggagagag accagctgag gcgtctctct ctgaggttgt gttgggtcta 1611

```
agcgggtgtg tgctgggctc caaggaggag gagcttgctg gggaaagaca ggagaagtac 1671

tgactcaact gcactgacca tgttgtcata attagaataa agaagaagtg gtcggaaatg 1731

cacattcctg gataggaatc acagctcacc ccaggatctc acaggtagtc tcctgagtag 1791

ttgacggcta gcggggagct agttccgccg catagttata gtgttgatgt gtgaacgctg 1851

acctgtcctg tgtgctaaga gctatgcagc ttagctgagg cgcctagatt actagatgtg 1911

ctgtatcacg gggaatgagg tgggggtgct tattttttaa tgaactaatc agagcctctt 1971

gagaaattgt tactcattga actggagcat caagacatct catggaagtg gatacggagt 2031

gatttggtgt ccatgctttt cactctgagg acatttaatc ggagaacctc ctggggaatt 2091

ttgtgggaga cacttgggaa caaaacagac accctgggaa tgcagttgca agcacagatg 2151

ctgccaccag tgtctctgac caccctggtg tgactgctga ctgccagcgt ggtacctccc 2211

atgctgcagg cctccatcta aatgagacaa caaagcacaa tgttcactgt ttacaaccaa 2271

gacaactgcg tgggtccaaa cactcctctt cctccaggtc atttgttttg catttttaat 2331

gtctttattt tttgtaatga aaaagcacac taagctgccc ctggaatcgg gtgcagctga 2391

ataggcaccc aaaagtccgt gactaaattt cgtttgtctt tttgatagca aattatgtta 2451

agagacagtg atggctaggg ctcaacaatt ttgtattccc atgtttgtgt gagacagagt 2511
```

ttgttttccc ttgaacttgg ttagaattgt gctactgtga acgctgatcc tgcatatgga 2571

agttccgctt cggtgacatt tcctggccat tcttgtttcc attgtgtgga tggtgggttg 2631

tgcccacttc ctggagtgag acagctcctg gtgtgtagaa ttcccggagc gtccgtggtt 2691

cagagtaaac ttgaagcaga tctgtgcatg cttttcctct gcaacaattg gctcgtttct 2751

cttttttgtt ctcttttgat aggatcctgt ttcctatgtg tgcaaaataa aaataaattt 2811

gggc 2815

<210> 168

<211> 172

<212> PRT

<213> Homo sapiens

<400> 168

Met Arg Arg Gln Pro Ala Lys Val Ala Ala Leu Leu Leu Gly Leu Leu
1   5   10   15

Leu Glu Cys Thr Glu Ala Lys Lys His Cys Trp Tyr Phe Glu Gly Leu
                20   25   30

Tyr Pro Thr Tyr Tyr Ile Cys Arg Ser Tyr Glu Asp Cys Cys Gly Ser
                35   40   45

出証特２００２－３０３２９３５

```
Arg Cys Cys Val Arg Ala Leu Ser Ile Gln Arg Leu Trp Tyr Phe Trp
    50                  55              60

Phe Leu Leu Met Met Gly Val Leu Phe Cys Cys Gly Ala Gly Phe Phe
    65              70              75                  80

Ile Arg Arg Arg Met Tyr Pro Pro Pro Leu Ile Glu Glu Pro Ala Phe
                85              90                  95

Asn Val Ser Tyr Thr Arg Gln Pro Pro Asn Pro Gly Pro Gly Ala Gln
                100             105             110

Gln Pro Gly Pro Pro Tyr Tyr Thr Asp Pro Gly Gly Pro Gly Met Asn
                115             120             125

Pro Val Gly Asn Ser Met Ala Met Ala Phe Gln Val Pro Pro Asn Ser
    130             135             140

Pro Gln Gly Ser Val Ala Cys Pro Pro Pro Ala Tyr Cys Asn Thr
145             150             155             160

Pro Pro Pro Pro Tyr Glu Gln Val Val Lys Ala Lys
                165             170
```

<210> 169

<211> 3337

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (136)..(1755)

<400> 169

tctcgctgcg ggaagggtcc tgggccccgg gcggcggtcg ccaggtctca gggccggggg 60

tacccgagtc tcgtttcctc tcagtccatc caccctttcat ggggccagag ccctctctcc 120

agaatctgag cagca atg ccg ttt gct gaa gac aag acc tat aag tat atc 171
              Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile
               1   5   10

tgc cgc aat ttc agc aat ttt tgc aat gtg gat gtt gta gag att ctg 219
Cys Arg Asn Phe Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu
     15   20   25

cct tac ctg ccc tgc ctc aca gca aga gac cag gat cga ctg cgg gcc 267
Pro Tyr Leu Pro Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala
     30   35   40

acc tgc aca ctc tca ggg aac cgg gac acc ctc tgg cat ctc ttc aat 315
Thr Cys Thr Leu Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn
     45   50   55   60

acc ctt cag cgg cgg ccc ggc tgg gtg gag tac ttc att gcg gca ctg 363
Thr Leu Gln Arg Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu

```
                65                          70                          75

agg ggc tgt gag cta gtt gat ctc gcg gac gaa gtg gcc tct gtc tac    411
Arg Gly Cys Glu Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr
                80                          85                          90


cag agc tac cag cct cgg acc tcg gac cgt ccc cca gac cca ctg gag    459
Gln Ser Tyr Gln Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu
            95                          100                         105


cca ccg tca ctt cct gct gag agg cca ggg ccc ccc aca cct gct gcg    507
Pro Pro Ser Leu Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala
        110                         115                         120


gcc cac agc atc ccc tac aac agc tgc aga gag aag gag cca agt tac    555
Ala His Ser Ile Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr
    125                         130                         135                         140


ccc atg cct gtc cag gag acc cag gcg cca gag tcc cca gga gag aat    603
Pro Met Pro Val Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn
                    145                         150                         155


tca gag caa gcc ctg cag acg ctc agc ccc aga gcc atc cca agg aat    651
Ser Glu Gln Ala Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn
                160                         165                         170


cca gat ggt ggc ccc ctg gag tcc tcc tct gac ctg gca gcc ctc agc    699
Pro Asp Gly Gly Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser
            175                         180                         185
```

```
cct ctg acc tcc agc ggg cat cag gag cag gac aca gaa ctg ggc agt     747
Pro Leu Thr Ser Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser
    190             195             200


acc cac aca gca ggt gcg acc tcc agc ctc aca cca tcc cgt ggg cct     795
Thr His Thr Ala Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro
205             210             215             220


gtg tct cca tct gtc tcc ttc cag ccc ctg gcc cgt tcc acc ccc agg     843
Val Ser Pro Ser Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg
            225             230             235


gca agc cgc ttg cct gga ccc aca ggg tca gtt gta tct act ggc acc     891
Ala Ser Arg Leu Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr
            240             245             250


tcc ttc tcc tcc tca tcc cct ggc ttg gcc tct gca ggg gct gca gag     939
Ser Phe Ser Ser Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu
            255             260             265


ggt aaa cag ggt gca gag agt gac cag gcc gag cct atc atc tgc tcc     987
Gly Lys Gln Gly Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser
    270             275             280


agt ggg gca gag gca cct gcc aac tct ctg ccc tcc aaa gtg cct acc     1035
Ser Gly Ala Glu Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr
285             290             295             300
```

```
acc ttg atg cct gtg aac aca gtg gcc ctg aaa gtg cct gcc aac cca      1083
Thr Leu Met Pro Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro
                305             310             315
```

```
gca tct gtc agc aca gtg ccc tcc aag ttg cca act agc tca aag ccc      1131
Ala Ser Val Ser Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro
                320             325             330
```

```
cct ggt gca gtg cct tct aat gcg ctc acc aat cca gca cca tcc aaa      1179
Pro Gly Ala Val Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys
                335             340             345
```

```
ttg ccc atc aac tca acc cgt gct ggc atg gtg cca tcc aaa gtg cct      1227
Leu Pro Ile Asn Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro
                350             355             360
```

```
act agc atg gtg ctc acc aag gtg tct gcc agc aca gtc ccc act gac      1275
Thr Ser Met Val Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp
365             370             375             380
```

```
ggg agc agc aga aat gag gag acc cca gca gct cca aca ccc gcc ggc      1323
Gly Ser Ser Arg Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly
                385             390             395
```

```
gcc act gga ggc agc tca gcc tgg cta gac agc agc tct gag aat agg      1371
Ala Thr Gly Gly Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg
                400             405             410
```

```
ggc ctt ggg tcg gag ctg agt aag cct ggc gtg ctg gca tcc cag gta      1419
```

```
Gly Leu Gly Ser Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val
        415             420             425
```

```
gac agc ccg ttc tcg ggc tgc ttc gag gat ctt gcc atc agt gcc agc     1467
Asp Ser Pro Phe Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser
        430             435             440
```

```
acc tcc ttg ggc atg ggg ccc tgc cat ggc cca gag gag aat gag tat     1515
Thr Ser Leu Gly Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr
 445             450             455             460
```

```
aag tcc gag ggc acc ttt ggg atc cac gtg gct gag aac ccc agc atc     1563
Lys Ser Glu Gly Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile
            465             470             475
```

```
cag ctc ctg gag ggc aac cct ggg cca cct gcg gac ccg gat ggc ggc     1611
Gln Leu Leu Glu Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly
        480             485             490
```

```
ccc agg cca caa gcc gac cgg aag ttc cag gag agg gag gtg cca tgc     1659
Pro Arg Pro Gln Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys
        495             500             505
```

```
cac agg ccc tca cct ggg gct ctg tgg ctc cag gtg gct gtg aca ggg     1707
His Arg Pro Ser Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly
        510             515             520
```

```
gtg ctg gta gtc aca ctc ctg gtg gtg ctg tac cgg cgg cgt ctg cac     1755
Val Leu Val Val Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
```

出証特２００２－３０３２９３５

525   530   535   540

```
tagtgaagcc ctgggctctt cccaccaccc atctgttccg ttcctgcagt atacctggcc 1815

cctctccgaa gcccctcttt ccctcccctc tggtctccat tctcttcagc tccctacatg 1875

ggctgggggag gagacacctg gtgggcagag ctcaggcaga ggtttggatt tcagctccct 1935

cacttccggg gctgtgtggc tttggcagat gtcagacttc tggtcttgct tctccacgtg 1995

gacagtgagt atctggctca ttcttcactg ggttcttctg agattgaacc tacaggtgtt 2055

tgccaagtgc ctggcccaga gcaagtggcc actgcttctc ccatctctct cctgcccaac 2115

ctggtagagc tgagggcatg agaggcagag tgcacagtgg tcaagggtgc agctctgcgg 2175

cacaggcagc ctaggcctgc gtcccaacct gcctctcacc agctctgtga ccttgggcaa 2235

gggatttatc tgtctgtccc ttagtttttct cacctgtaaa aggaggataa gtatatatat 2295

atatttccca gtgttgtgaa gattaaagga gtttatcgat gtaggtctta ggatgagtcc 2355

tggcatttac caagggttgg atatatgtta ttatcactat taagtgttga gggtccaggc 2415

atgctgggca acagggaccc catctctaca aaaaagttta aaaaattagc caggcgtggt 2475

ggtgcacctg tcgtcttagc tacttgggag gctgaggtgg gaggatcgct tgagcccgga 2535

agcttgaagc tgcagtgagc taggatcgtg ccactgcact ccaacctggg tgagagagcg 2595
```

```
agaccctgtc tcaagaaaaa gaaaaatgca gagaaacagg agtcttggct actcctttag 2655

aggcagactc agaccctcct gcctcacagc tttatctttg tatttgcccc ttactttatc 2715

ttgtgccttg agaaattgct ggggagagag gtatgtccac tgggcagctg tacaggatgg 2775

aggatatagg gcgtttccac tcccagcagc caggttccct cacccccaagc tcacccactg 2835

ttggggagat tatctacaat aacaccagaa acacattggg gtggattggg ggtatcctta 2895

tgggttcttt tcagggaacc attgctggac aaggcacagg agccacctcc atttctgagc 2955

tctgcaaggg acaagaacta gagccatcag gggctgggct cactgtggcc ccaccccaag 3015

ccgtcagcct ccagggatct acaccctgcc ttggctgcta cagctttttc actccactgc 3075

cctaggggag ttcagcaacc taatgatctc tatctctgaa catctcttca tcccatgctc 3135

caagtccagc aacctgcacc ctggaaccag gagtggaccc tacccgggct gtctgtatta 3195

atccccatcc cccaccacca atcttaaaaa gccctctgtc cccctaccct aaaccccagt 3255

taggtacccа tgctgggcag gtcagttaac aatttatgca caggtactag ttttattgta 3315

ttaccgttcc agggtagctt tg                                       3337
```

<210> 170

<211> 540

<212> PRT

<213> Homo sapiens

<400> 170

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

1   5   10   15

Ser Asn Phe Cys Asn Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro

            20   25   30

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu

        35   40   45

Ser Gly Asn Arg Asp Thr Leu Trp His Leu Phe Asn Thr Leu Gln Arg

    50   55   60

Arg Pro Gly Trp Val Glu Tyr Phe Ile Ala Ala Leu Arg Gly Cys Glu

65   70   75   80

Leu Val Asp Leu Ala Asp Glu Val Ala Ser Val Tyr Gln Ser Tyr Gln

                85   90   95

Pro Arg Thr Ser Asp Arg Pro Pro Asp Pro Leu Glu Pro Pro Ser Leu

                100   105   110

Pro Ala Glu Arg Pro Gly Pro Pro Thr Pro Ala Ala Ala His Ser Ile

                115   120   125

Pro Tyr Asn Ser Cys Arg Glu Lys Glu Pro Ser Tyr Pro Met Pro Val
130   135   140

Gln Glu Thr Gln Ala Pro Glu Ser Pro Gly Glu Asn Ser Glu Gln Ala
145   150   155   160

Leu Gln Thr Leu Ser Pro Arg Ala Ile Pro Arg Asn Pro Asp Gly Gly
                165   170   175

Pro Leu Glu Ser Ser Ser Asp Leu Ala Ala Leu Ser Pro Leu Thr Ser
                180   185   190

Ser Gly His Gln Glu Gln Asp Thr Glu Leu Gly Ser Thr His Thr Ala
                195   200   205

Gly Ala Thr Ser Ser Leu Thr Pro Ser Arg Gly Pro Val Ser Pro Ser
210   215   220

Val Ser Phe Gln Pro Leu Ala Arg Ser Thr Pro Arg Ala Ser Arg Leu
225   230   235   240

Pro Gly Pro Thr Gly Ser Val Val Ser Thr Gly Thr Ser Phe Ser Ser
                245   250   255

Ser Ser Pro Gly Leu Ala Ser Ala Gly Ala Ala Glu Gly Lys Gln Gly
                260   265   270

Ala Glu Ser Asp Gln Ala Glu Pro Ile Ile Cys Ser Ser Gly Ala Glu
                275   280   285

Ala Pro Ala Asn Ser Leu Pro Ser Lys Val Pro Thr Thr Leu Met Pro
    290   295   300

Val Asn Thr Val Ala Leu Lys Val Pro Ala Asn Pro Ala Ser Val Ser
305   310   315   320

Thr Val Pro Ser Lys Leu Pro Thr Ser Ser Lys Pro Pro Gly Ala Val
                325   330   335

Pro Ser Asn Ala Leu Thr Asn Pro Ala Pro Ser Lys Leu Pro Ile Asn
                340   345   350

Ser Thr Arg Ala Gly Met Val Pro Ser Lys Val Pro Thr Ser Met Val
                355   360   365

Leu Thr Lys Val Ser Ala Ser Thr Val Pro Thr Asp Gly Ser Ser Arg
    370   375   380

Asn Glu Glu Thr Pro Ala Ala Pro Thr Pro Ala Gly Ala Thr Gly Gly
385   390   395   400

Ser Ser Ala Trp Leu Asp Ser Ser Ser Glu Asn Arg Gly Leu Gly Ser
                405   410   415

Glu Leu Ser Lys Pro Gly Val Leu Ala Ser Gln Val Asp Ser Pro Phe
                420   425   430

Ser Gly Cys Phe Glu Asp Leu Ala Ile Ser Ala Ser Thr Ser Leu Gly

```
            435                440                445

Met Gly Pro Cys His Gly Pro Glu Glu Asn Glu Tyr Lys Ser Glu Gly
    450                455                460

Thr Phe Gly Ile His Val Ala Glu Asn Pro Ser Ile Gln Leu Leu Glu
465                470                475                480

Gly Asn Pro Gly Pro Pro Ala Asp Pro Asp Gly Gly Pro Arg Pro Gln
                485                490                495

Ala Asp Arg Lys Phe Gln Glu Arg Glu Val Pro Cys His Arg Pro Ser
            500                505                510

Pro Gly Ala Leu Trp Leu Gln Val Ala Val Thr Gly Val Leu Val Val
            515                520                525

Thr Leu Leu Val Val Leu Tyr Arg Arg Arg Leu His
            530                535                540
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<210> 171

<211> 3579

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (242)..(3094)

<400> 171

```
gtagtttcgg ctcggcagac ccggcgagcc cagtggccgc gctccggtgc ggcggcgccc   60

gaggcccgag gcggaagtgg gacggccaag cagggaagcg agggctcggg atcgacggcc  120

gcggggcgcc gacgaggagt gcaggactca ggaagggcga gtgcgcggcg acagagcccg  180

gggaaggagg cagggcaagg ccgggcttgg gggcaggtgg tccgggcatc cagccttgaa  240
```

```
g atg cac aag agg aaa gga ccc ccg gga ccc ccg ggc aga ggc gcc gcg   289
  Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala
  1               5                   10                  15
```

```
gcc gcc cgc cag ctg ggc ctg ctg gtt gac ctc tcc cca gat ggc ctg     337
Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu
            20                  25                  30
```

```
atg atc cct gag gac ggg gct aac gat gaa gaa ctg gag gct gag ttc     385
Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe
            35                  40                  45
```

```
ttg gct ttg gtc ggg ggc cag ccc cca gcc ctg gag aag ctc aaa ggc     433
Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly
        50                  55                  60
```

```
aaa ggt ccc ttg ccg atg gag gcc att gag aag atg gcc agc ctg tgc     481
Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys
```

```
              65                    70                    75                    80

atg aga gac ccg gat gag gat gag gag gag ggg acg gat gag gac gac      529
Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp
                          85                    90                    95

ttg gag gct gat gat gac ctg ctg gcg gag cta aat gag gtc ctt gga      577
Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
                  100                   105                   110

gag gag cag aag gct tca gag acc cca cct cct gtg gcc cag ccg aag      625
Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
          115                   120                   125

cct gag gcc cct cat ccg ggg ctg gag acc acc ttg cag gag agg ctg      673
Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
      130                   135                   140

gcg ctc tat cag aca gca att gaa agc gcc aga caa gct gga gac agc      721
Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
145                   150                   155                   160

gcc aag atg cgg cgc tac gat cgg ggg ctt aaa aca ctg gaa aac ctg      769
Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
                  165                   170                   175

ctc gcc tcc atc cgt aag ggc aat gcc att gac gaa gcg gac atc ccg      817
Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
                  180                   185                   190
```

```
ccg cca gtg gcc ata gga aaa ggc ccg gcg tcc acg cct acc tac agc    865
Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
         195                 200                 205


cct gca ccc acc cag ccg gcc cct aga atc gcg tca gcc cca gag ccc    913
Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
         210                 215                 220


agg gtc acc ctg gag gga cct tct gcc acc gcc cca gcc tca tct cca    961
Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225                 230                 235                 240


ggc ttg gct aag ccc cag atg ccc cca ggt ccc tgc agc cct ggc cct    1009
Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
                 245                 250                 255


ctg gcc cag ttg cag agc cgc cag cgc gac tac aag ctg gct gcc ctc    1057
Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
                 260                 265                 270


cac gcc aag cag cag gga gat acc act gct gcc gct aga cac ttc cgc    1105
His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
         275                 280                 285


gtg gct aag agc ttt gat gct gtc ttg gag gcc ctg agc cgg ggt gag    1153
Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
         290                 295                 300
```

```
ccc gtg gac ctc tcc tgc ctg ccc cct cca ccc gac cag ctg ccc cca    1201
Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Asp Gln Leu Pro Pro
305             310             315             320


gac cca ccg tca cca ccg tcg cag cct ccg acc ccc gct acg gcg ccc    1249
Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
                325             330             335


tcc aca aca gag gtg ccc cca ccc ccg agg acc ctg ctg gag gcg ctg    1297
Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
                340             345             350


gag cag cgg atg gag cgg tac cag gtg gcc gca gcc cag gcc aag agc    1345
Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
        355             360             365


aag ggg gac cag cgg aaa gct cga atg cac gag cgc atc gtc aag caa    1393
Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
    370             375             380


tac caa gat gcc atc cga gcc cac aag gct ggc cga gcc gtg gat gtc    1441
Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385             390             395             400


gct gaa ttg ccc gtg ccc cca ggc ttc ccc cca atc cag ggc ctg gag    1489
Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
                405             410             415


gcc acc aag ccc acc cag cag agt ctg gtg ggt gtc ctg gag act gcc    1537
```

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
        420   425   430

atg aag ctg gcc aac cag gat gaa ggc cca gag gat gaa gag gat gag   1585
Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
        435   440   445

gtg cct aag aag cag aac agc cct gtg gcc ccc aca gcc cag ccc aaa   1633
Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
        450   455   460

gcc cca ccc tca aga act ccc cag tcg gga tca gcc cca aca gcc aaa   1681
Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465   470   475   480

gcg ccc ccc aaa gcc aca tcc acc aga gcc cag cag cag ctg gcc ttc   1729
Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
           485   490   495

cta gag ggc cgc aag aag cag ctc ctg cag gcc gca ctg cga gcc aag   1777
Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
        500   505   510

cag aaa aac gac gtg gag ggt gcc aag atg cac ctg cgc caa gcc aag   1825
Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
        515   520   525

gga ctg gag cct atg ctg gag gcc tcg cgc aat ggg ctg cct gtg gac   1873
Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp

```
              530                    535                    540


atc acc aag gtg ccg cct gcc cct gtc aac aag gac gac ttt gcc ctg      1921
Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu
545                    550                    555                    560


gtc cag cgg cct ggc ccg ggt ctg tct cag gag gcc gcc cgg cgc tat      1969
Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
                       565                    570                    575


ggt gaa ctc acc aag ctc ata cgg cag cag cac gag atg tgc ctg aac      2017
Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
                       580                    585                    590


cac tca aac caa ttc acc cag ctg ggc aac atc act gaa acc acc aag      2065
His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
                       595                    600                    605


ttt gaa aag ttg gcg gag gac tgt aag cgg agc atg gac att ctg aag      2113
Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
                       610                    615                    620


caa gcc ttc gtc cgg ggt ctc ccc acg ccc acc gcc cgc ttt gag caa      2161
Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625                    630                    635                    640


agg acc ttc agc gtc atc aag atc ttc cct gac ctc agc agc aac gac      2209
Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
                       645                    650                    655
```

atg ctc ctc ttc atc gtg aag ggc atc aac ttg ccc aca ccc cca gga   2257
Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
          660   665   670

ctg tcc cct ggc gat ctg gat gtc ttt gtt cgg ttt gac ttc ccc tat   2305
Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
          675   680   685

ccc aac gtg gaa gaa gct cag aaa gac aag acc agt gtg atc aag aac   2353
Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
    690   695   700

aca gac tcc cct gag ttc aag gag cag ttc aaa ctc tgc atc aac cgc   2401
Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705   710   715   720

agc cac cgt ggc ttc cga agg gcc atc cag acc aag ggc atc aag ttc   2449
Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
          725   730   735

gaa gtg gtt cac aag ggg ggg ctg ttc aag act gac cgg gtg ctg ggg   2497
Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
          740   745   750

aca gcc cag ctg aag ctg gat gca ctg gag ata gca tgt gag gtc cgg   2545
Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
          755   760   765

gag atc ctt gag gtc ctg gat ggt cgc cgg ccc aca ggg ggg cga ctg　　　2593
Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
　　770　　　　　　　775　　　　　　　780

gag gta atg gtc cgg att cgg gag cca ctg aca gcc cag cag ttg gag　　　2641
Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
　　785　　　　　　　790　　　　　　　795　　　　　　　800

acg acg aca gag agg tgg ctg gtc att gac cct gtg ccg gca gct gtg　　　2689
Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
　　　　　　　805　　　　　　　810　　　　　　　815

ccc aca cag gtt gct ggg ccc aaa ggg aag gcc cct cct gtg cct gcc　　　2737
Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
　　　　　　　820　　　　　　　825　　　　　　　830

cct gca agg gag tca ggg aac aga tca gcc cgg ccc ctg cat agc ctc　　　2785
Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
　　　　　　　835　　　　　　　840　　　　　　　845

agt gtg ctg gcg ttt gac caa gag cgt ctg gag cgg aag atc ctg gcc　　　2833
Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
　　850　　　　　　　855　　　　　　　860

ctc agg cag gcg cgg cgg ccg gtg ccc cca gaa gtg gcc cag cag tac　　　2881
Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
　　865　　　　　　　870　　　　　　　875　　　　　　　880

cag gac atc atg caa cgc agc cag tgg cag agg gca cag ctg gag cag　　　2929

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
             885   890   895

ggg ggt gtg ggc atc cga cgg gaa tac aca gcc cag ctg gag cgg cag   2977
Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
             900   905   910

ctg cag ttc tac acg gag gct gcc cgg cgc ctg ggc aac gat ggc agc   3025
Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
             915   920   925

agg gat gct gca aag gag gcg ctc tat agg cgg aat ctg gta ggg agt   3073
Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
        930   935   940

gag ctg cag cgg ctc cgc agg tgaggagccc atggggcggg cagcccccag   3124
Glu Leu Gln Arg Leu Arg Arg
945   950

aaagcgggca gcaggccccg ataccgggaa gagccgacac agccacgaac cagacaagca 3184

gacaatcagc ggacaatcgg ttctggactc acccctcatc cgggccccca gccccgccag 3244

agcctccgtg gctgcgggtg ttgggaacca tgcctgccag ccagtatgtg cccctcaccc 3304

aggcctggct gggccctgga gagtcctgtt tgcacagccc aggggtgtcc ggcctctggc 3364

ccgcccccgga gcagggaggg cggctggggc caagccccga gggcccctgc aagcacttta 3424

cttcctgttc ctccccagcc ttaaccccaa agccctcctg caccccaaag aagccactga 3484

ggctggccga gccacactgt ctccccaggg gcgtcgacct ggcccagctg ggtccccagg 3544

ccagcacatg gaataaaata gccagggcca cactc   3579

<210> 172

<211> 951

<212> PRT

<213> Homo sapiens

<400> 172

Met His Lys Arg Lys Gly Pro Pro Gly Pro Pro Gly Arg Gly Ala Ala

1   5   10   15

Ala Ala Arg Gln Leu Gly Leu Leu Val Asp Leu Ser Pro Asp Gly Leu

            20   25   30

Met Ile Pro Glu Asp Gly Ala Asn Asp Glu Glu Leu Glu Ala Glu Phe

        35   40   45

Leu Ala Leu Val Gly Gly Gln Pro Pro Ala Leu Glu Lys Leu Lys Gly

    50   55   60

Lys Gly Pro Leu Pro Met Glu Ala Ile Glu Lys Met Ala Ser Leu Cys

65   70   75   80

Met Arg Asp Pro Asp Glu Asp Glu Glu Glu Gly Thr Asp Glu Asp Asp

                85   90   95

Leu Glu Ala Asp Asp Asp Leu Leu Ala Glu Leu Asn Glu Val Leu Gly
                100   105   110

Glu Glu Gln Lys Ala Ser Glu Thr Pro Pro Pro Val Ala Gln Pro Lys
                115   120   125

Pro Glu Ala Pro His Pro Gly Leu Glu Thr Thr Leu Gln Glu Arg Leu
                130   135   140

Ala Leu Tyr Gln Thr Ala Ile Glu Ser Ala Arg Gln Ala Gly Asp Ser
     145   150   155   160

Ala Lys Met Arg Arg Tyr Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu
                     165   170   175

Leu Ala Ser Ile Arg Lys Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro
                180   185   190

Pro Pro Val Ala Ile Gly Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser
                195   200   205

Pro Ala Pro Thr Gln Pro Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro
     210   215   220

Arg Val Thr Leu Glu Gly Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro
225   230   235   240

Gly Leu Ala Lys Pro Gln Met Pro Pro Gly Pro Cys Ser Pro Gly Pro
            245   250   255

Leu Ala Gln Leu Gln Ser Arg Gln Arg Asp Tyr Lys Leu Ala Ala Leu
            260   265   270

His Ala Lys Gln Gln Gly Asp Thr Thr Ala Ala Ala Arg His Phe Arg
            275   280   285

Val Ala Lys Ser Phe Asp Ala Val Leu Glu Ala Leu Ser Arg Gly Glu
            290   295   300

Pro Val Asp Leu Ser Cys Leu Pro Pro Pro Asp Gln Leu Pro Pro
305   310   315   320

Asp Pro Pro Ser Pro Pro Ser Gln Pro Pro Thr Pro Ala Thr Ala Pro
            325   330   335

Ser Thr Thr Glu Val Pro Pro Pro Pro Arg Thr Leu Leu Glu Ala Leu
            340   345   350

Glu Gln Arg Met Glu Arg Tyr Gln Val Ala Ala Ala Gln Ala Lys Ser
            355   360   365

Lys Gly Asp Gln Arg Lys Ala Arg Met His Glu Arg Ile Val Lys Gln
            370   375   380

Tyr Gln Asp Ala Ile Arg Ala His Lys Ala Gly Arg Ala Val Asp Val
385   390   395   400

Ala Glu Leu Pro Val Pro Pro Gly Phe Pro Pro Ile Gln Gly Leu Glu
      405   410   415

Ala Thr Lys Pro Thr Gln Gln Ser Leu Val Gly Val Leu Glu Thr Ala
      420   425   430

Met Lys Leu Ala Asn Gln Asp Glu Gly Pro Glu Asp Glu Glu Asp Glu
      435   440   445

Val Pro Lys Lys Gln Asn Ser Pro Val Ala Pro Thr Ala Gln Pro Lys
    450   455   460

Ala Pro Pro Ser Arg Thr Pro Gln Ser Gly Ser Ala Pro Thr Ala Lys
465   470   475   480

Ala Pro Pro Lys Ala Thr Ser Thr Arg Ala Gln Gln Gln Leu Ala Phe
      485   490   495

Leu Glu Gly Arg Lys Lys Gln Leu Leu Gln Ala Ala Leu Arg Ala Lys
      500   505   510

Gln Lys Asn Asp Val Glu Gly Ala Lys Met His Leu Arg Gln Ala Lys
      515   520   525

Gly Leu Glu Pro Met Leu Glu Ala Ser Arg Asn Gly Leu Pro Val Asp
      530   535   540

Ile Thr Lys Val Pro Pro Ala Pro Val Asn Lys Asp Asp Phe Ala Leu

545   550   555   560

Val Gln Arg Pro Gly Pro Gly Leu Ser Gln Glu Ala Ala Arg Arg Tyr
              565   570   575

Gly Glu Leu Thr Lys Leu Ile Arg Gln Gln His Glu Met Cys Leu Asn
         580   585   590

His Ser Asn Gln Phe Thr Gln Leu Gly Asn Ile Thr Glu Thr Thr Lys
         595   600   605

Phe Glu Lys Leu Ala Glu Asp Cys Lys Arg Ser Met Asp Ile Leu Lys
    610   615   620

Gln Ala Phe Val Arg Gly Leu Pro Thr Pro Thr Ala Arg Phe Glu Gln
625   630   635   640

Arg Thr Phe Ser Val Ile Lys Ile Phe Pro Asp Leu Ser Ser Asn Asp
         645   650   655

Met Leu Leu Phe Ile Val Lys Gly Ile Asn Leu Pro Thr Pro Pro Gly
         660   665   670

Leu Ser Pro Gly Asp Leu Asp Val Phe Val Arg Phe Asp Phe Pro Tyr
         675   680   685

Pro Asn Val Glu Glu Ala Gln Lys Asp Lys Thr Ser Val Ile Lys Asn
    690   695   700

Thr Asp Ser Pro Glu Phe Lys Glu Gln Phe Lys Leu Cys Ile Asn Arg
705   710   715   720

Ser His Arg Gly Phe Arg Arg Ala Ile Gln Thr Lys Gly Ile Lys Phe
            725   730   735

Glu Val Val His Lys Gly Gly Leu Phe Lys Thr Asp Arg Val Leu Gly
            740   745   750

Thr Ala Gln Leu Lys Leu Asp Ala Leu Glu Ile Ala Cys Glu Val Arg
            755   760   765

Glu Ile Leu Glu Val Leu Asp Gly Arg Arg Pro Thr Gly Gly Arg Leu
            770   775   780

Glu Val Met Val Arg Ile Arg Glu Pro Leu Thr Ala Gln Gln Leu Glu
785   790   795   800

Thr Thr Thr Glu Arg Trp Leu Val Ile Asp Pro Val Pro Ala Ala Val
                805   810   815

Pro Thr Gln Val Ala Gly Pro Lys Gly Lys Ala Pro Pro Val Pro Ala
            820   825   830

Pro Ala Arg Glu Ser Gly Asn Arg Ser Ala Arg Pro Leu His Ser Leu
            835   840   845

Ser Val Leu Ala Phe Asp Gln Glu Arg Leu Glu Arg Lys Ile Leu Ala
            850   855   860

Leu Arg Gln Ala Arg Arg Pro Val Pro Pro Glu Val Ala Gln Gln Tyr
865   870   875   880

Gln Asp Ile Met Gln Arg Ser Gln Trp Gln Arg Ala Gln Leu Glu Gln
        885   890   895

Gly Gly Val Gly Ile Arg Arg Glu Tyr Thr Ala Gln Leu Glu Arg Gln
        900   905   910

Leu Gln Phe Tyr Thr Glu Ala Ala Arg Arg Leu Gly Asn Asp Gly Ser
        915   920   925

Arg Asp Ala Ala Lys Glu Ala Leu Tyr Arg Arg Asn Leu Val Gly Ser
        930   935   940

Glu Leu Gln Arg Leu Arg Arg
945   950

<210> 173

<211> 2796

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (574)..(1683)

<400> 173

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ttgggccttt tcttgtgtcc tgtttgttaa aggcatgcgg gctccagcat taaagagggc  120

tagtccttaa caaagggaaa gcgataaatg taaataagct cacattttca gaatgagcgg  180

tttgcagtaa ggagctgcgg cagcccagag tctgctcttt ttgggctggg ctaacctttc  240

cctgtttttt gtttttttgtt ttgttttgtt tttgtttttt atggataaaa atatgcgctt  300

ccgaagtgcg agttgccagt ttacacgttt attagctaac tatctacagg catgagcaca  360

ttctctcatc tagcacactc tttcttgggc actcaattga ggaactctct gatcgtctgc  420

ctccagaaaa ttcattgatt atccaagtct cagataaatc tggtgccaga gtttggtttg  480

aactaactaa tgaagaaagc attctctact ggtcctcagt ctcaagagtg gtgaacccct  540

gcacctagca ggctctctgg gaaaaaaaaa tcc atg ggt gac aga aga ttt att  594
                                    Met Gly Asp Arg Arg Phe Ile
                                     1               5

gac ttc caa ttc caa gat tta aat tca agt ctc aga ccc agg ttg gga  642
Asp Phe Gln Phe Gln Asp Leu Asn Ser Ser Leu Arg Pro Arg Leu Gly
        10              15              20

aat gca act gcc aat aat act tgc att gtt gat gat tcc ttc aag tat  690
```

Asn Ala Thr Ala Asn Asn Thr Cys Ile Val Asp Asp Ser Phe Lys Tyr
　　　25　　　　　　　　　　30　　　　　　　　　　35

aat ttg aat ggt gct gtc tat agt gtt gta ttc atc ctg ggt cta ata　　738
Asn Leu Asn Gly Ala Val Tyr Ser Val Val Phe Ile Leu Gly Leu Ile
　　　40　　　　　　　　　　45　　　　　　　　　　50　　　　　　　　　　55

acc aac agt gcc tcc ctg ttt gtc ttc tgc ttc cgc atg aaa atg aga　　786
Thr Asn Ser Ala Ser Leu Phe Val Phe Cys Phe Arg Met Lys Met Arg
　　　　　　　　　　　　　　60　　　　　　　　　　65　　　　　　　　　　70

agt gag acg gct act ttc atc acc aac ctg gcc ctc tct gat ttg ctt　　834
Ser Glu Thr Ala Thr Phe Ile Thr Asn Leu Ala Leu Ser Asp Leu Leu
　　　　　　　　　　75　　　　　　　　　　80　　　　　　　　　　85

ttt gtt tgt acc cta cct ttc aaa ata ttt tac aac ttt aat cgc cac　　882
Phe Val Cys Thr Leu Pro Phe Lys Ile Phe Tyr Asn Phe Asn Arg His
　　　　　　　　90　　　　　　　　　　95　　　　　　　　　　100

tgg cct ttt ggt gac acc ctc tgt aag atc tca ggg act gcg ttc ctc　　930
Trp Pro Phe Gly Asp Thr Leu Cys Lys Ile Ser Gly Thr Ala Phe Leu
　　　　　　　105　　　　　　　　　　110　　　　　　　　　　115

acc aac atc tat ggg agc atg ctc ttc ctc acc tgc atc agt gtg gat　　978
Thr Asn Ile Tyr Gly Ser Met Leu Phe Leu Thr Cys Ile Ser Val Asp
　　120　　　　　　　　　　125　　　　　　　　　　130　　　　　　　　　　135

cgt ttc cta gcc att gtc tat ccc ttc cga tcg cgt acc atc agg acc　　1026
Arg Phe Leu Ala Ile Val Tyr Pro Phe Arg Ser Arg Thr Ile Arg Thr

```
              140                    145                      150

agg agg aat tcc gcc att gtg tgc gct gga gtc tgg atc cta gtc ctc   1074
Arg Arg Asn Ser Ala Ile Val Cys Ala Gly Val Trp Ile Leu Val Leu
        155                    160                    165

agt ggt ggt att tca gct tct ttg ttc tcc acc act aat gtc aac aat   1122
Ser Gly Gly Ile Ser Ala Ser Leu Phe Ser Thr Thr Asn Val Asn Asn
        170                    175                    180

gcg acc acc act tgc ttt gaa ggc ttc tcc aaa cgt gtc tgg aag aca   1170
Ala Thr Thr Thr Cys Phe Glu Gly Phe Ser Lys Arg Val Trp Lys Thr
        185                    190                    195

tac ctg tcc aag atc act ata ttc att gaa gtt gtt gga ttc atc att   1218
Tyr Leu Ser Lys Ile Thr Ile Phe Ile Glu Val Val Gly Phe Ile Ile
200                    205                    210                    215

cct ctg ata ttg aat gtt tct tgt tct tct gtg gtg ctt aga acc ctc   1266
Pro Leu Ile Leu Asn Val Ser Cys Ser Ser Val Val Leu Arg Thr Leu
        220                    225                    230

cgc aag cct gca aca ttg tct cag att ggg acc aat aag aaa aaa gtg   1314
Arg Lys Pro Ala Thr Leu Ser Gln Ile Gly Thr Asn Lys Lys Lys Val
        235                    240                    245

ttg aag atg atc aca gtg cat atg gca gtg ttt gtg gta tgc ttt gta   1362
Leu Lys Met Ile Thr Val His Met Ala Val Phe Val Val Cys Phe Val
        250                    255                    260
```

```
cca tac aac tcc gtt ctc ttt tta tat gcc ttg gta cgc tcc caa gcc    1410
Pro Tyr Asn Ser Val Leu Phe Leu Tyr Ala Leu Val Arg Ser Gln Ala
    265             270             275


att act aat tgc tta ttg gaa agg ttt gca aag atc atg tac cca att    1458
Ile Thr Asn Cys Leu Leu Glu Arg Phe Ala Lys Ile Met Tyr Pro Ile
280             285             290             295


acc ttg tgc ctt gca act ctg aat tgt tgc ttt gat cct ttt atc tat    1506
Thr Leu Cys Leu Ala Thr Leu Asn Cys Cys Phe Asp Pro Phe Ile Tyr
            300             305             310


tac ttc act ctt gaa tcc ttt cag aag tcc ttt tat atc aat aca cat    1554
Tyr Phe Thr Leu Glu Ser Phe Gln Lys Ser Phe Tyr Ile Asn Thr His
            315             320             325


ata agg atg gag tcg ctg ttt aag act gag aca cct ctg acc ccc aaa    1602
Ile Arg Met Glu Ser Leu Phe Lys Thr Glu Thr Pro Leu Thr Pro Lys
            330             335             340


cct tcc ctt cca gct atc caa gag gaa gtt agt gat caa aca aca aat    1650
Pro Ser Leu Pro Ala Ile Gln Glu Glu Val Ser Asp Gln Thr Thr Asn
    345             350             355


aat ggt ggt gaa tta atg ctg gaa tcc acc ttc taggtaccag aattgtcttt 1703
Asn Gly Gly Glu Leu Met Leu Glu Ser Thr Phe
360             365             370
```

caggttcagc tacagtgtct cttatgattt ttttcctatg ctataaatag gagaaacaaa 1763

ttgaagctaa tgatactgag aatagagtaa tgtaccaaat gcagtcagat acatttgttt 1823

gaacactatt gtacatattc tgttttgttc agtaattata ggtcaagtct aattacaaca 1883

accaaaacag atcagcctct tctgttgagt tgacttttca ttacctaaat gaccagtggt 1943

cttgactttt agtgatgtga gggttatttt taaacttaaa aaaaaggca ttccagtaat 2003

tttggtaatt gggttgggcc tataaatata gaacaaattc agggattatt taaaaacatc 2063

tgtgttacta ctgatatatg ctagtatttt tttccttttt tgaattaata ttgaatttat 2123

tttaaaaaaa gaactatttt tacctaatct taataagaca tactgagaaa gagaaatgtg 2183

ttgaatttta aaatattggc aaattttacc tagattttaa aaacctaaat gaagtgtttg 2243

aatgaatatg ggtgggaaat ttggaattta gacaacattt acgcatttat aataaccaca 2303

attagtgtca gcttttaaaa ctttcttttt aaaataattc tagaattttc atatgaaatt 2363

gttaatcctg aaaggtgcta cttatgtgcc tggcaggtat aaaatggaaa actcataaaa 2423

ttaacagtgt caatttaaaa aaaaaaaaac tttaagcaac actatattat ttcttaagat 2483

tttcatttat cctttatggg ggtggggatt ggcttgtaga aaatatttat tcttcatgtt 2543

aaatgttggg gacacattac agccagagag ctacagtatt tgtgcccagg tcaggagtaa 2603

attgaaaaag taagtgaata gaatagtagc agcaagatat cttagagctt atattagtag 2663

tttttaaggt ggtggttaga tagctgtaat tttgaaatcc atactctctt ctgtacattt 2723

tggagcacat tgtagccaag gcgctgctga atttgtgctc aggtcgggag catattgaaa 2783

aagatgtgta cat   2796

<210> 174

<211> 370

<212> PRT

<213> Homo sapiens

<400> 174

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Leu Asn Ser
1   5   10   15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
                20   25   30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
                35   40   45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Ala Ser Leu Phe Val Phe
            50   55   60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Thr Phe Ile Thr Asn

```
         65                    70                    75                    80
```

Leu Ala Leu Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile

```
                    85                    90                    95
```

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys

```
              100                   105                   110
```

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe

```
              115                   120                   125
```

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe

```
         130                   135                   140
```

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala

```
   145                   150                   155                   160
```

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe

```
                    165                   170                   175
```

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe

```
              180                   185                   190
```

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile

```
         195                   200                   205
```

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser

```
   210                   215                   220
```

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
            245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
            260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Leu Leu Glu Arg Phe
            275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
            290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   315   320

Ser Phe Tyr Ile Asn Thr His Ile Arg Met Glu Ser Leu Phe Lys Thr
            325   330   335

Glu Thr Pro Leu Thr Pro Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
            340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
            355   360   365

Thr Phe
370

<210> 175

<211> 2299

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)..(1176)

<400> 175

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aagtcc atg ggt gac aga aga ttc att gac ttc caa ttc caa gat tca   108
       Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser
        1   5   10

aat tca agc ctc aga ccc agg ttg ggc aat gct act gcc aat aat act   156
Asn Ser Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr
15   20   25   30

tgc att gtt gat gat tcc ttc aag tat aat ctc aat ggt gct gtc tac   204
Cys Ile Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr
         35   40   45

agt gtt gta ttc atc ttg ggt ctg ata acc aac agt gtc tct ctg ttt   252
Ser Val Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe

```
                50                    55                    60

gtc ttc tgt ttc cgc atg aaa atg aga agt gag act gct att ttt atc   300
Val Phe Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile
        65                    70                    75


acc aat cta gct gtc tct gat ttg ctt ttt gtc tgt aca cta cct ttt   348
Thr Asn Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe
        80                    85                    90


aaa ata ttt tac aac ttc aac cgc cac tgg cct ttt ggt gac acc ctc   396
Lys Ile Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu
    95                    100                   105                   110


tgc aag atc tct gga act gca ttc ctt acc aac atc tat ggg agc atg   444
Cys Lys Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met
                115                   120                   125


ctc ttt ctc acc tgt att agt gtg gat cgt ttc ctg gcc att gtc tat   492
Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr
                130                   135                   140


cct ttt cga tct cgt act att agg act agg agg aat tct gcc att gtg   540
Pro Phe Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val
                145                   150                   155


tgt gct ggt gtc tgg atc cta gtc ctc agt ggc ggt att tca gcc tct   588
Cys Ala Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser
                160                   165                   170
```

出証特２００２−３０３２９３５

```
ttg ttt tcc acc act aat gtc aac aat gca acc acc acc tgc ttt gaa    636
Leu Phe Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu
175             180             185             190


ggc ttc tcc aaa cgt gtc tgg aag act tat tta tcc aag atc aca ata    684
Gly Phe Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile
            195             200             205


ttt att gaa gtt gtt ggg ttt atc att cct cta ata ttg aat gtc tct    732
Phe Ile Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser
            210             215             220


tgc tct tct gtg gtg ctg aga act ctt cgc aag cct gct act ctg tct    780
Cys Ser Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser
            225             230             235


caa att ggg acc aat aag aaa aaa gta ctg aaa atg atc aca gta cat    828
Gln Ile Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His
            240             245             250


atg gca gtc ttt gtg gta tgc ttt gta ccc tac aac tct gtc ctc ttc    876
Met Ala Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe
255             260             265             270


ttg tat gcc ctg gtg cgc tcc caa gct att act aat tgc ttt ttg gaa    924
Leu Tyr Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu
            275             280             285
```

```
aga ttt gca aag atc atg tac cca atc acc ttg tgc ctt gca act ctg    972
Arg Phe Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu
          290             295             300


aac tgt tgt ttt gac cct ttc atc tat tac ttc acc ctt gaa tcc ttt    1020
Asn Cys Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe
          305             310             315


cag aag tcc ttc tac atc aat gcc cac atc aga atg gag tcc ctg ttt    1068
Gln Lys Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe
      320             325             330


aag act gaa aca cct ttg acc aca aag cct tcc ctt cca gct att caa    1116
Lys Thr Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln
335             340             345             350


gag gaa gtg agt gat caa aca aca aat aat ggt ggt gaa tta atg cta    1164
Glu Glu Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu
              355             360             365


gaa tcc acc ttt taggtatgag aaatgtgttc aggtccagat atggtttctc        1216
Glu Ser Thr Phe
              370


ctataatttt tcctatgcta taaactaaag atttgaagct aatgatactg agaataatgc  1276

accaaatcca gtcagataca tttgtttgaa ggtatactgt agagttttta ttgctgtttt  1336

gttcagtaat tataggtcaa atctaattac aacaaccaag atggattgcc aaactcttct  1396
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```
gcttggttgg aatttcattg tatcgcatta tccaggtggc tagtggcatt tgataatata 1456

gagatgactt tgaaactttc aaaaaggtat ttctattcca atgatatttg gtaattaggt 1516

tgggcctata aatatagaac aaattcaggg atttttaaaa aattgtgtta ctactgatat 1576

atgctagttt tattttattt ttttggactg tcattgagtt tattttagca caagaatatt 1636

tttagcctaa cattattaat aagaaatgtg tcaatttttt aacattggta aaatatgtta 1696

tgtgcatttt gaaaacagaa aacaaattgc gttggcatgt acgtgggtgg gaagaaaaag 1756

aaaattaaca ggatttacac aattataatc accagcagtg tgagtttaaa aaacttcgtt 1816

gttttacac caaattaaaa ttttcatgtc aaacttcaaa gccagaaagc tgctaaatac 1876

gtgtctggca ggtaaaagct ggaaaattac ttaaaacagg aaagtgtcaa taaaaaaact 1936

tgagcaacac caacatattt tttcttaaaa tgtcacgtta tcttcatttt gggaaactag 1996

gttctataaa atatttatcc tccctgttat actttggagc acagcacagc cagaaagggg 2056

ctgcatttgt gcccaggtca ggagcaaatt gaaaaaaaaa ataaagtaat actaaaaaat 2116

caaactataa acccaaaaca tttattaaaa cctgaattaa ccttttttgg agggaggagt 2176

agagatatat aacctgaaaa tacttattct ttcttatcga attttggagc ctaatatagc 2236
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caggagctgc tgaatttgtg cccctggatt ggaaccaaat aaaaaaaaaa aaaaaaaatt 2296

cct 2299

<210> 176

<211> 370

<212> PRT

<213> Homo sapiens

<400> 176

Met Gly Asp Arg Arg Phe Ile Asp Phe Gln Phe Gln Asp Ser Asn Ser
1   5   10   15

Ser Leu Arg Pro Arg Leu Gly Asn Ala Thr Ala Asn Asn Thr Cys Ile
                20   25   30

Val Asp Asp Ser Phe Lys Tyr Asn Leu Asn Gly Ala Val Tyr Ser Val
                35   40   45

Val Phe Ile Leu Gly Leu Ile Thr Asn Ser Val Ser Leu Phe Val Phe
    50   55   60

Cys Phe Arg Met Lys Met Arg Ser Glu Thr Ala Ile Phe Ile Thr Asn
65   70   75   80

Leu Ala Val Ser Asp Leu Leu Phe Val Cys Thr Leu Pro Phe Lys Ile
                85   90   95

Phe Tyr Asn Phe Asn Arg His Trp Pro Phe Gly Asp Thr Leu Cys Lys
              100   105   110

Ile Ser Gly Thr Ala Phe Leu Thr Asn Ile Tyr Gly Ser Met Leu Phe
              115   120   125

Leu Thr Cys Ile Ser Val Asp Arg Phe Leu Ala Ile Val Tyr Pro Phe
              130   135   140

Arg Ser Arg Thr Ile Arg Thr Arg Arg Asn Ser Ala Ile Val Cys Ala
145   150   155   160

Gly Val Trp Ile Leu Val Leu Ser Gly Gly Ile Ser Ala Ser Leu Phe
              165   170   175

Ser Thr Thr Asn Val Asn Asn Ala Thr Thr Thr Cys Phe Glu Gly Phe
              180   185   190

Ser Lys Arg Val Trp Lys Thr Tyr Leu Ser Lys Ile Thr Ile Phe Ile
              195   200   205

Glu Val Val Gly Phe Ile Ile Pro Leu Ile Leu Asn Val Ser Cys Ser
     210   215   220

Ser Val Val Leu Arg Thr Leu Arg Lys Pro Ala Thr Leu Ser Gln Ile
225   230   235   240

Gly Thr Asn Lys Lys Lys Val Leu Lys Met Ile Thr Val His Met Ala
              245   250   255

Val Phe Val Val Cys Phe Val Pro Tyr Asn Ser Val Leu Phe Leu Tyr
   260   265   270

Ala Leu Val Arg Ser Gln Ala Ile Thr Asn Cys Phe Leu Glu Arg Phe
   275   280   285

Ala Lys Ile Met Tyr Pro Ile Thr Leu Cys Leu Ala Thr Leu Asn Cys
   290   295   300

Cys Phe Asp Pro Phe Ile Tyr Tyr Phe Thr Leu Glu Ser Phe Gln Lys
305   310   315   320

Ser Phe Tyr Ile Asn Ala His Ile Arg Met Glu Ser Leu Phe Lys Thr
   325   330   335

Glu Thr Pro Leu Thr Thr Lys Pro Ser Leu Pro Ala Ile Gln Glu Glu
   340   345   350

Val Ser Asp Gln Thr Thr Asn Asn Gly Gly Glu Leu Met Leu Glu Ser
   355   360   365

Thr Phe
  370

<210> 177

<211> 973

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (30)..(416)

<400> 177

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                                   Met Ala Arg Gly Ser Leu Arg Arg
                                    1               5


ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg ctg gcg ttg ctg cgc tcc     101
Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
     10              15                  20


gtg gcc ggg gag caa gcg cca ggc acc gcc ccc tgc tcc cgc ggc agc     149
Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
 25              30                  35                  40


tcc tgg agc gcg gac ctg gac aag tgc atg gac tgc gcg tct tgc agg     197
Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
                 45                  50                  55


gcg cga ccg cac agc gac ttc tgc ctg ggc tgc gct gca gca cct cct     245
Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
                 60                  65                  70


gcc ccc ttc cgg ctg ctt tgg ccc atc ctt ggg ggc gct ctg agc ctg     293
```

```
Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
        75              80              85
```

```
acc ttc gtg ctg ggg ctg ctt tct ggc ttt ttg gtc tgg aga cga tgc    341
Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
        90              95              100
```

```
cgc agg aga gag aag ttc acc acc ccc ata gag gag acc ggc gga gag    389
Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
105             110             115             120
```

```
ggc tgc cca gct gtg gcg ctg atc cag tgacaatgtg ccccctgcca           436
Gly Cys Pro Ala Val Ala Leu Ile Gln
                125
```

```
gccggggctc gcccactcat cattcattca tccattctag agccagtctc tgcctcccag  496
```

```
acgcggcggg agccaagctc ctccaaccac aaggggggtg ggggcggtg aatcacctcc  556
```

```
gaggcctggg tccagggttc aggggaacct tccaaggtgt ctggttgccc tgcctctggc  616
```

```
tccagaacag aaagggagcc tcacgctggc tcacacaaaa cagctgacac tgactaagga  676
```

```
actgcagcat ttgcacaggg gaggggggtg ccctccttcc tagaggccct gggggccagg  736
```

```
ctgacttggg gggcagactt gacactaggc cccactcact cagatgtcct gaaattccac  796
```

```
cacggggggtc accctggggg gttagggacc tattttttaac actagggggc tggcccacta  856
```

ggagggctgg ccctaagata cagacccccc caactcccca aagcggggag gagatattta 916

ttttggggag agtttggagg ggagggagaa tttattaata aaagaatctt taacttt 973

<210> 178

<211> 129

<212> PRT

<213> Homo sapiens

<400> 178

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Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly
1               5                  10                  15


Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
                20                  25                  30


Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
            35                  40                  45


Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
        50                  55                  60


Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
65                  70                  75                  80


Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
                    85                  90                  95
```

Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
        100   105   110

Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
        115   120   125

Gln

<210> 179

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 179

cttctgctct aaaagctgcg   20

<210> 180

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 180

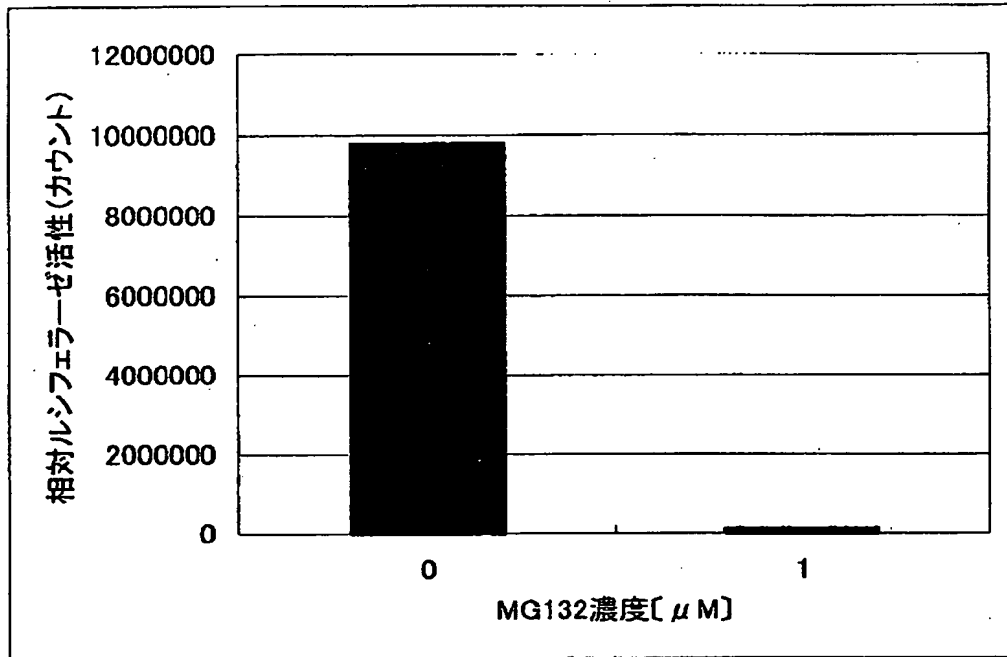cgacctgcag ctcgagcaca   20

　　　【０１２９】

　　　【配列表フリーテキスト】

配列番号１７９：プライマー

配列番号１８０：プライマー

【図面の簡単な説明】

　　　【図１】

　図１は、実施例３のプロテアソーム阻害剤ＭＧ１３２によるＮＦ－κＢのレポ
ーター活性抑制を示す図である。図中で横軸は、ＭＧ１３２濃度、縦軸は、相対
ルシフェラーゼ活性を示す。

【書類名】　　　図面

【図１】

相対ルシフェラーゼ活性（カウント）

MG132濃度〔μM〕

【書類名】　　　　要約書

【要約】

【課題】　　　ＮＦ－κＢの過剰な活性化または阻害が関与する疾患の診断、治療または予防等に使用されるＮＦ－κＢ作用を有するタンパク質の提供。

【解決手段】　　　ヒト肺線維芽細胞から作製したｃＤＮＡライブラリーから、プラスミドｐＮＦκＢ－Ｌｕｃを用いて、ＮＦ－κＢを活性化する作用を有するタンパク質をコードするｃＤＮＡをクローニングして、そのＤＮＡ配列およびそれより推定されるアミノ酸配列を決定した。同タンパク質、これをコードするＤＮＡ，同ＤＮＡを含有する組換えベクターおよび同組換えベクターを含有する形質転換体は、ＮＦ－κＢの活性化を阻害または促進する物質のスクリーニングに使用される。

【選択図】　　　なし

【書類名】　　　　　　手続補正書

【整理番号】　　　　　X13-994

【提出日】　　　　　　平成13年11月12日

【あて先】　　　　　　特許庁長官　殿

【事件の表示】

　　【出願番号】　　　特願2001-254018

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　　【識別番号】　　　100091096

　　【弁理士】

　　【氏名又は名称】　平木　祐輔

【手続補正　　1】

　　【補正対象書類名】　特許願

　　【補正対象項目名】　発明者

　　【補正方法】　　　変更

　　【補正の内容】

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　　　　　　　　　　　　　出証特２００２−３０３２９３５

【氏名】　　　　　　本田　剛一

【プルーフの要否】　要

認定 ・ 付加情報

特許出願の番号	特願２００１－２５４０１８
受付番号	５０１０１６６３７６９
書類名	手続補正書
担当官	森吉　美智枝　　　　　７５７７
作成日	平成１３年１２月２０日

＜認定情報・付加情報＞
【補正をする者】
　　　【識別番号】　　　　　000000033
　　　【住所又は居所】　　　大阪府大阪市北区堂島浜１丁目２番６号
　　　【氏名又は名称】　　　旭化成株式会社
　【代理人】　　　　　　　　申請人
　　　【識別番号】　　　　　100091096
　　　【住所又は居所】　　　東京都港区虎ノ門１丁目１７番１号　虎ノ門５森
　　　　　　　　　　　　　　ビル３階平木国際特許事務所
　　　【氏名又は名称】　　　平木　祐輔

出 願 人 履 歴 情 報

識別番号 〔０００００００３３〕

1. 変更年月日 ２００１年 １月 ４日
   [変更理由] 名称変更
   住 所 大阪府大阪市北区堂島浜１丁目２番６号
   氏 名 旭化成株式会社